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From: Lacourciere, Karen
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(703) 308-7523
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Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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AA Sequences: _____
Structures: _____
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
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DRLink: _____
Lexis/Nexis: _____
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SEARCH REQUEST FORM

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 22

Search Site
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_____ DARC/Questel
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L1 (FILE 'REGISTRY' ENTERED AT 10:55:53 ON 13 JAN 2003)
20 S TTTCAACCAGATGGTCATTC/SQSN

L2 FILE 'HCAPLUS' ENTERED AT 10:57:04 ON 13 JAN 2003
7 S L1

L2 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:889441 HCAPLUS

DOCUMENT NUMBER: 137:381006

TITLE: Expressed sequence profiles and their use for
the therapy and diagnosis of human lung cancer
INVENTOR(S): Henderson, Robert A.; Wang, Tongtong; Watanabe,
Yoshihiro; Johnson, Jeffrey C.; Retter, Marc W.;
Durham, Margarita; Carter, Darrick; Fanger, Gary
R.; Vedvick, Thomas S.; Bangur, Chaitanya S.;
McNabb, Andria

PATENT ASSIGNEE(S): Corixa Corporation, USA

SOURCE: U.S. Pat. Appl. Publ., 82 pp., Cont.-in-part of
U.S. Ser. No. 849,626.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002172952	A1	20021121	US 2001-902941	20010710
US 6504010	B1	20030107	US 2000-702705	20001030
US 2002168637	A1	20021114	US 2000-736457	20001213
US 2002197669	A1	20021226	US 2001-849626	20010503

PRIORITY APPLN. INFO.:

US 1999-419356	A2	19990630
US 1999-346492	A2	19991015
US 1999-466867	A2	19991217
US 1999-476300	A2	19991230
US 2000-519642	A2	20000306
US 2000-533077	A2	20000322
US 2000-546259	A2	20000410
US 2000-560406	A2	20000427
US 2000-589184	A2	20000605
US 2000-614124	A2	20000711
US 2000-651563	A2	20000829
US 2000-658824	A2	20000908
US 2000-671325	A2	20000926
US 2000-677419	A2	20001006
US 2000-702705	A2	20001030
US 2000-736457	A2	20001213
US 2001-849626	A2	20010503
WO 2000-US18061	A2	20000630

AB Nucleic acid and encoded protein compns. and methods for the therapy
and diagnosis of cancer, particularly lung cancer, are disclosed.
Thus, cDNAs encoding tumor-assocd. proteins were identified by
conventional and PCR-based library subtraction, cDNA microarray
anal., and real-time PCR using cDNA libraries isolated from lung
adenocarcinoma, small cell lung carcinoma, squamous cell lung
carcinoma, and lung neuroendocrine carcinoma vs. a pool of poly(A)+
RNA from 9 normal tissues. Illustrative compns. comprise one or
more lung tumor polypeptides, immunogenic portions thereof,

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polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compns. are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

IT 475864-34-7

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (nucleotide sequence; expressed sequence profiles and their use for the therapy and diagnosis of human lung cancer)

L2 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:869469 HCAPLUS

DOCUMENT NUMBER: 137:364446

TITLE: Expressed sequence profiles and their use for the therapy and diagnosis of human lung cancer

INVENTOR(S): Wang, Tongtong; Bangur, Chaitanya S.; Lodes, Michael J.; Fanger, Gary R.; Vedvick, Thomas S.; Carter, Darrick; Retter, Marc W.; Mannion, Jane; Fan, Liqun; Wang, Aijun

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 66 pp., Cont.-in-part of U. S. Ser. No. 702,705.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002168637	A1	20021114	US 2000-736457	20001213
WO 2001000828	A3	20010802	WO 2000-US18061	20000630
WO 2001000828	A2	20010104		
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RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1196565	A2	20020417	EP 2000-945031	20000630
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
BR 2000012069	A	20020827	BR 2000-12069	20000630
US 6504010	B1	20030107	US 2000-702705	20001030
US 2002197669	A1	20021226	US 2001-849626	20010503
US 2002172952	A1	20021121	US 2001-902941	20010710
WO 2002004514	A2	20020117	WO 2001-US22058	20020710
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR,			

Searcher : Shears 308-4994

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TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ,
MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD,
TG

PRIORITY APPLN. INFO.:

US 1999-346492	A2 19990630
US 1999-419356	A2 19991015
US 1999-466867	A2 19991217
US 1999-476300	A2 19991230
US 2000-519642	A2 20000306
US 2000-533077	A2 20000322
US 2000-546259	A2 20000410
US 2000-560406	A2 20000427
US 2000-589184	A2 20000605
WO 2000-US18061	A2 20000630
US 2000-614124	A2 20000711
US 2000-651563	A2 20000829
US 2000-658824	A2 20000908
US 2000-671325	A2 20000926
US 2000-677419	A2 20001006
US 2000-702705	A2 20001030
US 2000-736457	A2 20001213
US 2001-849626	A2 20010503

AB Nucleic acid and encoded protein compns. and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Thus, cDNAs encoding tumor-assocd. proteins were identified by conventional and PCR-based library subtraction, cDNA microarray anal., and real-time PCR using cDNA libraries isolated from lung adenocarcinoma, small cell lung carcinoma, squamous cell lung carcinoma, and lung neuroendocrine carcinoma vs. a pool of poly(A)+ RNA from 9 normal tissues. Illustrative compns. comprise one or more lung tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compns. are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

IT 475019-40-0

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(nucleotide sequence; expressed sequence profiles and their use for the therapy and diagnosis of human lung cancer)

L2 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:332807 HCAPLUS

DOCUMENT NUMBER: 136:351185

TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.;
Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto,
Italo A.; Briones, Marcelo R. S.; Costa,
Fernando F.; Nagai, Maria Aparecida;
Verjovski-Almeida, Sergio; Zago, Marco A.;
Andrade, Luis Eduardo C.; Carrer, Helaine;
El-Dorry, Hamza F. A.; Espreafico, Enilza M.;
Habr-Gama, Angelita; Giannella-Neto, Daniel;

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Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Lilliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalcborg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estd. that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000

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ORESTES generated are derived from transcripts from an estd. 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstr. record is one of many records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 270220-29-6, GenBank AW992843 270220-33-2, GenBank AW992847

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

L2 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:332795 HCAPLUS

DOCUMENT NUMBER: 136:351174

TITLE: The contribution of 700,000 ORF sequence tags to the definition of the human transcriptome

AUTHOR(S): Camargo, Anamaria A.; Samaia, Helena P. B.; Dias-Neto, Emmanuel; Simao, Daniel F.; Migotto, Italo A.; Briones, Marcelo R. S.; Costa, Fernando F.; Nagai, Maria Aparecida; Verjovski-Almeida, Sergio; Zago, Marco A.; Andrade, Luis Eduardo C.; Carrer, Helaine; El-Dorry, Hamza F. A.; Espreafico, Enilza M.; Habr-Gama, Angelita; Giannella-Neto, Daniel; Goldman, Gustavo H.; Gruber, Arthur; Hackel, Christine; Kimura, Edna T.; Maciel, Rui M. B.; Marie, Suely K. N.; Martins, Elizabeth A. L.; Nobrega, Marina P.; Paco-Larson, Maria Luisa; Pardini, Maria Ines M. C.; Pereira, Goncalo G.; Pesquero, Joao Bosco; Rodrigues, Vanderlei; Rogatto, Silvia R.; Da Silva, Ismael D. C. G.; Sogayar, Mari C.; Sonati, Maria De Fatima; Tajara, Eloiza H.; Valentini, Sandro R.; Alberto, Fernando L.; Amaral, Maria Elisabete J.; Aneas, Ivy; Arnaldi, Liliane A. T.; De Assis, Angela M.; Bengtson, Mario Henrique; Bergamo, Nadia Aparecida; Bombonato, Vanessa; De Camargo, Maria E. R.; Canevari, Renata A.; Carraro, Dirce M.; Cerutti, Janete M.; Correa, Maria Lucia C.; Correa, Rosana F. R.; Costa, Maria Cristina R.; Curcio, Cyntia; Hokama, Paula O. M.; Ferreira, Ari J. S.; Furuzawa, Gilberto K.; Gushiken, Tsieko; Ho, Paulo L.; Kimura, Elza; Krieger, Jose E.; Leite, Luciana C. C.; Majumder, Paromita; Marins, Mozart; Marques, Everaldo R.; Melo, Analy S. A.; Melo, Monica; Mestriner, Carlos Alberto; Miracca, Elisabete C.; Miranda, Daniela C.; Nascimento, Ana Lucia

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T. O.; Nobrega, Francisco G.; Ojopi, Elida P. B.; Pandolfi, Jose Rodrigo C.; Pessoa, Luciana G.; Prevedel, Aline C.; Rahal, Paula; Rainho, Claudia A.; Reis, Eduardo M. R.; Ribeiro, Marcelo L.; Da Ros, Nancy; De Sa, Renata G.; Sales, Magaly M.; Sant'anna, Simone Cristina; Dos Santos, Mariana L.; Da Silva, Aline M.; Da Silva, Neusa P.; Silva, Wilson A., Jr.; Da Silveira, Rosana A.; Sousa, Josane F.; Stecconi, Daniella; Tsukumo, Fernando; Valente, Valeria; Soares, Fernando; Moreira, Eloisa S.; Nunes, Diana N.; Correa, Ricardo G.; Zalberg, Heloisa; Carvalho, Alex F.; Reis, Luis F. L.; Brentani, Ricardo R.; Simpson, Andrew J. G.; De Souza, Sandro J.

CORPORATE SOURCE: Ludwig Institute for Cancer Research, Sao Paulo, 01509-010, Brazil

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2001), 98(21), 12103-12108

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Open reading frame expressed sequences tags (ORESTES) differ from conventional ESTs by providing sequence data from the central protein coding portion of transcripts. A total of 696,745 ORESTES sequences were generated from 24 human tissues and a subset of the data that correspond to a set of 15,095 full-length mRNAs used as a means of assessing the efficiency of the strategy and its potential contribution to the definition of the human transcriptome. It was estd. that ORESTES sampled over 80% of all highly and moderately expressed, and between 40% and 50% of rarely expressed, human genes. In the most thoroughly sequenced tissue, the breast, the 130,000 ORESTES generated are derived from transcripts from an estd. 70% of all genes expressed in that tissue, with an equally efficient representation of both highly and poorly expressed genes. In this respect, the capacity of the ORESTES strategy both for gene discovery and shotgun transcript sequence generation significantly exceeds that of conventional ESTs. The distribution of ORESTES is such that many human transcripts are now represented by a scaffold of partial sequences distributed along the length of each gene product. The exptl. joining of the scaffold components, by reverse transcription-PCR, represents a direct route to transcript finishing that may represent a useful alternative to full-length cDNA cloning. [This abstr. record is one of many records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 272727-43-2, GenBank BE092864

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; contribution of 700,000 ORF sequence tags to the definition of the human transcriptome)

L2 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:51525 HCAPLUS

DOCUMENT NUMBER: 136:129944

TITLE: Human nucleic acid and expressed protein

Searcher : Shears 308-4994

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INVENTOR(S): compositions and methods for the therapy and diagnosis of lung cancer
Wang, Tongtong; Watanabe, Yoshihiro; Henderson, Robert A.; Johnson, Jeffrey C.; Retter, Marc W.; Marnerakis, Margarita; Carter, Darrick; Fanger, Gary Richard; Vedvick, Thomas S.; Bangur, Chaitanya S.; McNabb, Andria; Wang, Aijun; Fanger, Neil; Switzer, Ann; McNeill, Patricia D.; Clapper, Jonathan D.
PATENT ASSIGNEE(S): Corixa Corporation, USA
SOURCE: PCT Int. Appl., 223 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002004514	A2	20020117	WO 2001-US22058	20020710
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
US 6504010	B1	20030107	US 2000-702705	20001030
US 2002168637	A1	20021114	US 2000-736457	20001213
US 2002197669	A1	20021226	US 2001-849626	20010503
PRIORITY APPLN. INFO.:			US 2000-614124	A 20000711
			US 2000-651563	A 20000829
			US 2000-658824	A 20000908
			US 2000-671325	A 20000926
			US 2000-677419	A 20001006
			US 2000-702705	A 20001030
			US 2000-736457	A 20001213
			US 2001-849626	A 20010503
			US 1999-419356	B2 19990630
			US 1999-346492	A2 19991015
			US 1999-466867	A2 19991217
			US 1999-476300	A2 19991230
			US 2000-519642	A2 20000306
			US 2000-533077	A2 20000322
			US 2000-546259	A2 20000410
			US 2000-560406	A2 20000427
			US 2000-589184	A2 20000605
			WO 2000-US18061	A2 20000630
AB	Compns. and methods for the therapy and diagnosis of cancer, particularly lung cancer, are disclosed. Illustrative compns. comprise one or more lung tumor polypeptides, immunogenic portions thereof, the cDNA polynucleotides that encode such polypeptides, antigen-presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides.			

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Thus, lung tumor cDNAs are isolated and characterized using conventional cDNA library subtraction, PCR-based subtraction, microarray anal., and lung chip 5. The cDNA libraries are isolated from lung adenocarcinoma, small cell lung carcinoma, lung neuroendocrine carcinoma, and squamous cell lung carcinoma. The immunogenic gene products are expressed in Escherichia coli, and epitope mapping is provided using antibodies one of the lung tumor-specific antigens, designated L552S. The disclosed compns. are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly lung cancer.

IT 388152-61-2P

RL: ANT (Analyte); BPN (Biosynthetic preparation); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses) (nucleotide sequence; human nucleic acid and expressed protein compns. and methods for the therapy and diagnosis of lung cancer)

L2 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:731174 HCAPLUS

DOCUMENT NUMBER: 135:283933

TITLE: Nucleic acid markers and methods for the measurement of sensitivity or resistance to agents used in identification, assessment, prevention, and therapy of human cancers

INVENTOR(S): Lillie, James; Brown, Jeffrey L.; Bolt, Andrew; Van Huffel, Christophe

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 223 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001073430	A2	20011004	WO 2001-US9202	20010322
WO 2001073430	A3	20020411		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

US 2002081596 A1 20020627 US 2001-816292 20010322

PRIORITY APPLN. INFO.: US 2000-192100P P 20000324

US 2000-197064P P 20000413

AB The present invention is directed to the identification of markers that can be used to det. whether cancer cells are sensitive or resistant to a therapeutic agent. The present invention is also directed to the identification of therapeutic targets. The invention features 436 "sensitivity markers". These are markers that are expressed in most or all cell lines that are sensitive to

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treatment with an agent and which are not expressed (or are expressed at a rather low level) in cells that are resistant to treatment with that agent. The invention also features 3132 "resistance markers". These are markers that are expressed in most or all cell lines that are resistant to treatment with an agent and which are not expressed (or are expressed at a rather low level) in cells that are sensitive to treatment with that agent. PCR-based subtractive hybridization of cDNA libraries from normal and cancerous tissues was used to identify the markers. At least some of the examples relate to sensitivity or resistance to taxol.

IT 191206-39-0

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)

(resistance marker; nucleic acid markers and methods for the measurement of sensitivity or resistance to agents used in identification, assessment, prevention, and therapy of human cancers)

L2 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:551387 HCAPLUS

DOCUMENT NUMBER: 135:103496

TITLE: Nucleic acid compositions, kits, and methods for identification, assessment, prevention, and therapy of human breast cancer

INVENTOR(S): Lillie, James; Palermo, Adam; Wang, Youzhen; Steinmann, Kathleen; Elias, Josh

PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA

SOURCE: PCT Int. Appl., 2674 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001046697	A2	20010628	WO 2000-US35214	20001221
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR			
PRIORITY APPLN. INFO.:			US 1999-PV171406	19991221
			US 2000-PV176423	20000114
			US 2000-PV190471	20000317
			US 2000-PV193482	20000329
			US 2000-PV205231	20000515
			US 2000-PV213236	20000620
			US 2000-PV219865	20000720

AB The invention relates to nucleic acid marker comps., kits and methods for detecting, characterizing, preventing, and treating human breast cancers. A variety of markers are provided, wherein changes in the levels of expression of one or more of the nucleic acid markers is correlated with the presence of breast cancer. The

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level of expression of numerous potential markers was measured in cells obtained from breast cancer tissue samples obtained from fifteen patients afflicted with breast cancer and from eleven breast cancer cell cultures, based on comparison with expression levels of each marker in corresponding non-cancerous breast tissue and cell cultures. The 15 cancer tissue samples include (i) five invasive lobular carcinomas (ILC), (ii) five invasive ductal carcinomas (IDC), and (iii) five samples of ductal carcinoma in situ (DCIS). As an addnl. evaluation of ability to indicate breast cancer, individual markers that were identified by transcriptional profiling criteria were also tested in six different subtracted library expts. In addn., protein profiling expts. were undertaken to assess whether the proteins assocd. with the expression of individual markers of the invention are secreted. Table 21 lists approx. 43,500 GenBank Accession Nos. from the present invention. [This abstr. record is two of eight records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 191206-39-0

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; nucleic acid compns., kits, and methods for identification, assessment, prevention, and therapy of human breast cancer)

E61 THROUGH E67 ASSIGNED

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L3 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN 475864-34-7 REGISTRY

CN DNA (human clone R0127:G07 lung tumor-associated protein cDNA fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 981: PN: US20020172952 SEQID: 981 claimed DNA

SQL 550

MF Unspecified

CI MAN

REFERENCE 1: 137:381006

L3 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN 475019-40-0 REGISTRY

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OTHER NAMES:

CN 981: PN: US20020168637 SEQID: 981 claimed DNA

SQL 550

MF Unspecified

CI MAN

REFERENCE 1: 137:364446

L3 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN 388152-61-2 REGISTRY

Searcher : Shears 308-4994

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09/757100

CN DNA (human clone B0127:G07 lung tumor-associated protein cDNA
fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 979: PN: WO0204514 SEQID: 981 claimed DNA

SQL 550

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CI MAN

REFERENCE 1: 136:129944

L3 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN **272727-43-2** REGISTRY

CN DNA (human clone CM2-BT0741-050400-140-c12 EST (expressed sequence
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OTHER NAMES:

CN GenBank BE092864

SQL 412

MF Unspecified

CI MAN

REFERENCE 1: 136:351174

L3 ANSWER 5 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN **270220-33-2** REGISTRY

CN DNA (human clone RC2-BN0032-120200-011-d08 EST (expressed sequence
tag)) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AW992847

SQL 682

MF Unspecified

CI MAN

REFERENCE 1: 136:351185

L3 ANSWER 6 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN **270220-29-6** REGISTRY

CN DNA (human clone RC2-BN0032-120200-011-b08 EST (expressed sequence
tag)) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AW992843

SQL 648

MF Unspecified

CI MAN

REFERENCE 1: 136:351185

L3 ANSWER 7 OF 7 REGISTRY COPYRIGHT 2003 ACS

RN **191206-39-0** REGISTRY

CN DNA (human clone 795352 EST (expressed sequence tag)) (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN 1216: PN: WO0173430 TABLE: 2 claimed DNA

CN 4606: PN: WO0146697 TABLE: 21 claimed DNA

SQL 598

MF Unspecified

CI MAN

REFERENCE 1: 135:283933

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REFERENCE 2: 135:103496

FILE 'HOME' ENTERED AT 10:58:05 ON 13 JAN 2003

Searcher : Shears 308-4994

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 09:46:50 ; Search time 3165 Seconds
(without alignments)
158.878 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	20	29	US-09-757-100B-18
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C 5	20	100.0	325	19	US-09-515-694-6610
C 6	20	100.0	379	17	US-09-359-067-23180
C 7	20	100.0	416	38	US-10-007-926A-284
C 8	20	100.0	421	31	US-09-824-557-1277
C 9	20	100.0	433	30	US-09-790-435-4313
C 10	20	100.0	436	16	US-09-289-768-4292
C 11	20	100.0	436	35	US-09-939-397-4292
C 12	20	100.0	443	18	US-09-431-517-3422
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ALIGNMENTS

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PCT-US00-18999-18
; Sequence 18, Application PC/TUS0018999
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0476
; CURRENT APPLICATION NUMBER: PCT/US00/18999
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US00-18999-18

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-377-310-18
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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310A
; CURRENT FILING DATE: 1999-08-19
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; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-18
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 18, Application US/09757100B
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-18
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; GENERAL INFORMATION:
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; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-754CON1
; CURRENT APPLICATION NUMBER: US/09/332,782
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: US 09/181,430
; EARLIER FILING DATE: 1998-10-28
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6610
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US-09-332-782-6610

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; APPLICANT: Cheung, Patrick
; APPLICANT: Damavandi, Simin
; APPLICANT: Dickson, Mark
; APPLICANT: Drake, Jim
; APPLICANT: Drmanac, Radoje
; APPLICANT: Engleman, Carrie
; APPLICANT: Faulkner, Brandy
; APPLICANT: Fox, Melvin
; APPLICANT: Garcia, Veronica
; APPLICANT: Giedt, Gretchen
; APPLICANT: Jomek, Leni
; APPLICANT: Jones, Lee
; APPLICANT: Kita, David
; APPLICANT: Kofler, Janette
; APPLICANT: Labat, Ivan
; APPLICANT: Lee, Won-Jae
; APPLICANT: Lomelli, Michelle
; APPLICANT: Nguyen, Hong
; APPLICANT: Nguyen, Linh
; APPLICANT: Nguyen, Lynne
; APPLICANT: Nguyen, Phuong
; APPLICANT: Nogra, Margie
; APPLICANT: Ojeda, Jesse
; APPLICANT: Palencia, Servando
; APPLICANT: Rasi, Fariba
; APPLICANT: Randhwa, Gurpreet
; APPLICANT: Sanourieh, Hannah
; APPLICANT: Sidhu, Navjwan
; APPLICANT: Smith, Benjamin
; APPLICANT: Smythe, Ashleigh
; APPLICANT: Tkach, Joe
; APPLICANT: Tulpule, Mukul
; APPLICANT: Verna, Ron
; APPLICANT: Wachter, Adam
; APPLICANT: Wu, James
; APPLICANT: Yim, Kenneth
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 754CIP
; CURRENT APPLICATION NUMBER: US/09/515,694
; CURRENT FILING DATE: 2000-02-29
; EARLIER APPLICATION NUMBER: 09/332,782
; EARLIER FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/181,430
; EARLIER FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 21027
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6610
; LENGTH: 325
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-515-694-6610

Query Match 100.0%; Score 20; DB 19; Length 325;
Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
|||||
DB 53 TTTCACACGATGGTCATTC 34

RESULT 6

US-09-359-067-23180/c
; Sequence 23180, Application US/09359067
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-747CON1
; CURRENT APPLICATION NUMBER: US/09/359,067
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/131,598
; EARLIER FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 49786
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23180
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-359-067-23180

Query Match 100.0%; Score 20; DB 17; Length 379;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
|||||
DB 339 TTTCACACGATGGTCATTC 320

RESULT 7

US-10-007-926A-284/c
; Sequence 284, Application US/10007926A
; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 284
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 5' terminal sequence. ptk2 protein tyrosine
; OTHER INFORMATION: kinase 2 (PTK2) gene.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (275)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (295)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (364)

; OTHER INFORMATION: a, t, c or g
US-10-007-926A-284

Query Match 100.0%; Score 20; DB 38; Length 416;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
|||||
Db 343 TTTCACCGAGATGTCATTC 324

RESULT 8
US-09-824-557-1277/C
; Sequence 1277, Application US/09824557
; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2086-001
; CURRENT APPLICATION NUMBER: US/09/824,557
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,438
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9773
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1277
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(421)
; OTHER INFORMATION: n = A,T,C or G
US-09-824-557-1277

Query Match 100.0%; Score 20; DB 31; Length 421;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
|||||
Db 270 TTTCACCGAGATGTCATTC 251

RESULT 9
US-09-790-435-4313/C

; Sequence 4313, Application US/09790435
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2060-001
; CURRENT APPLICATION NUMBER: US/09/790,435
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/183,730
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 7473
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4313
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(433)
; OTHER INFORMATION: n = A,T,C or G
US-09-790-435-4313

Query Match 100.0%; Score 20; DB 30; Length 433;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
|||||
Db 200 TTTCACCGAGATGTCATTC 181

RESULT 10
US-09-289-768-4292/C
; Sequence 4292, Application US/09289768
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4292
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(436)
; OTHER INFORMATION: n = A,T,C or G
US-09-289-768-4292

Query Match 100.0%; Score 20; DB 16; Length 436;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
|||||
Db 97 TTTCACCGAGATGTCATTC 78

RESULT 11
US-09-939-397-4292/C

; Sequence 4292, Application US/09939397
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/939,397
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/289,768
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4292
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(436)
; OTHER INFORMATION: n = A,T,C or G
US-09-939-397-4292

Query Match 100.0%; Score 20; DB 35; Length 436;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
|||||
Db 97 TTTCACCGAGATGTCATTC 78

RESULT 12
US-09-431-517-3422/C
; Sequence 3422, Application US/09431517


```
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-751CON1
; CURRENT APPLICATION NUMBER: US/09/431,517
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: US 09/170,294
; EARLIER FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 31760
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3422
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(443)
; OTHER INFORMATION: n = A,T,C or G
US-09-431-517-3422
```

```
Query Match 100.0%; Score 20; DB 18; Length 443;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTCACACAGATGGTCATTC 20
Db 73 TTTCACACAGATGGTCATTC 54
```

```
RESULT 13
US-09-306-350A-30669/c
; Sequence 30669, Application US/09306350A
; GENERAL INFORMATION:
; APPLICANT: Dickson, Mark C.
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Jones, Lee W.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 20411-776
; CURRENT APPLICATION NUMBER: US/09/306,350A
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 41304
; SOFTWARE: pt CT_1 Version 1.1
; SEQ ID NO 30669
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-350A-30669
```

```
Query Match 100.0%; Score 20; DB 17; Length 449;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTCACACAGATGGTCATTC 20
Db 208 TTTCACACAGATGGTCATTC 189
```

```
RESULT 14
US-09-909-629-30669/c
; Sequence 30669, Application US/09909629
; GENERAL INFORMATION:
; APPLICANT: Dickson, Mark C.
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Jones, Lee W.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; FILE REFERENCE: 20411-776
```

```
; CURRENT APPLICATION NUMBER: US/09/909,629
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/306,350
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 41304
; SOFTWARE: pt CT_1 Version 1.1
; SEQ ID NO 30669
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-909-629-30669
```

```
Query Match 100.0%; Score 20; DB 34; Length 449;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTCACACAGATGGTCATTC 20
Db 208 TTTCACACAGATGGTCATTC 189
```

```
RESULT 15
US-09-824-557-3555/c
; Sequence 3555, Application US/09824557
; GENERAL INFORMATION:
; APPLICANT: Stryjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2086-001
; CURRENT APPLICATION NUMBER: US/09/824,557
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,438
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9773
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3555
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: n = A,T,C or G
US-09-824-557-3555
```

```
Query Match 100.0%; Score 20; DB 31; Length 455;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTCACACAGATGGTCATTC 20
Db 266 TTTCACACAGATGGTCATTC 247
```

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Search completed: January 12, 2003, 12:04:06
Job time : 3167 secs
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 09:51:30 ; Search time 168 Seconds
(without alignments)
110.212 Million cell updates/sec

Title: US-09-757-100B-18

Perfect score: 20
Sequence: 1 ttccaaccagatgggtcattc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2355679 seqs, 462891617 residues

Total number of hits satisfying chosen parameters: 4711358

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*

- 1: /cgn2_6/prodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/prodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/prodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/prodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	550	1	PCT-US02-34777-981
2	20	100.0	550	6	US-10-283-017-981
3	20	100.0	1317	5	US-09-724-676-20756
4	20	100.0	1317	5	US-09-724-676-20756
5	20	100.0	1362	5	US-09-724-676-20755
6	20	100.0	1362	5	US-09-724-676-20755
7	20	100.0	1791	5	US-09-724-676-20750
8	20	100.0	1791	5	US-09-724-676-20750
9	20	100.0	1836	5	US-09-724-676-20749
10	20	100.0	1836	5	US-09-724-676-20749
11	20	100.0	3610	5	US-09-724-676-20752
12	20	100.0	3610	5	US-09-724-676-20752
13	20	100.0	3677	5	US-09-724-676-20751
14	20	100.0	3677	5	US-09-724-676-20751
15	20	100.0	3697	5	US-09-724-676-20754
16	20	100.0	3697	5	US-09-724-676-20754
17	20	100.0	3764	5	US-09-724-676-20753
18	20	100.0	3764	5	US-09-724-676-20753
19	20	100.0	4371	5	US-09-724-676-20759
20	20	100.0	4371	5	US-09-724-676-20759
21	20	100.0	4438	5	US-09-724-676-20758
22	20	100.0	4438	5	US-09-724-676-20758
23	20	100.0	4458	5	US-09-724-676-20748
24	20	100.0	4458	5	US-09-724-676-20748
25	20	100.0	4481	5	US-10-240-965-92
26	20	100.0	4525	5	US-09-724-676-20760

ALIGNMENTS

RESULT 1

PCT-US02-34777-981

; Sequence 981, Application PC/TUS0234777

; GENERAL INFORMATION:

; APPLICANT: Corixa Corporation

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Kalos, Michael D.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Johnson, Jeffrey C.

; APPLICANT: Retter, Marc W.

; APPLICANT: Durham, Margarita

; APPLICANT: Carter, Darick

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.47803PC

; CURRENT APPLICATION NUMBER: PCT/US02/34777

; NUMBER OF SEQ ID NOS: 2157

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 981

; LENGTH: 550

; TYPE: DNA

; ORGANISM: Homo sapiens

PCT-US02-34777-981

Query Match 100.0%; Score 20; DB 1; Length 550;

Best Local Similarity 100.0%; Pred. No. 0.47;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACAGATGGTCATTC 20

|||||

Db 195 TTTCACACAGATGGTCATTC 214

RESULT 2

US-10-283-017-981

; Sequence 981, Application US/10283017

; GENERAL INFORMATION:

; APPLICANT: Henderson, Robert A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Kalos, Michael D.

; APPLICANT: Sleath, Paul R.

```

; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margalita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 981
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-017-981
```

```
Query Match          100.0%; Score 20; DB 6; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TTTCAACCGATGGTCATTC 20
|||||
Db 195 TTTCAACCGATGGTCATTC 214
```

```

RESULT 3
US-09-724-676-20756/c
; Sequence 20756, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20756
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20756
```

```
Query Match          100.0%; Score 20; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TTTCAACCGATGGTCATTC 20
|||||
Db 372 TTTCAACCGATGGTCATTC 353
```

```

RESULT 4
US-09-724-676A-20756/c
; Sequence 20756, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20756
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20756
```

```
Query Match          100.0%; Score 20; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TTTCAACCGATGGTCATTC 20
|||||
Db 372 TTTCAACCGATGGTCATTC 353
```

```

RESULT 5
US-09-724-676-20755/c
; Sequence 20755, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20755
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20755
```

```
Query Match          100.0%; Score 20; DB 5; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TTTCAACCGATGGTCATTC 20
|||||
Db 417 TTTCAACCGATGGTCATTC 398
```

```

RESULT 6
US-09-724-676A-20755/c
; Sequence 20755, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20755
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20755
```

```
Query Match          100.0%; Score 20; DB 5; Length 1362;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 1 TTTCAACCGATGGTCATTC 20
|||||
Db 417 TTTCAACCGATGGTCATTC 398
```

```

RESULT 7
US-09-724-676-20750/c
; Sequence 20750, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20750
```

```
;
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20750

Query Match      100.0%; Score 20; DB 5; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 846 TTTCACCAACGATGGTCATTC 827

RESULT 8
US-09-724-676A-20750/c
; Sequence 20750, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20750
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20750

Query Match      100.0%; Score 20; DB 5; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

*QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 846 TTTCACCAACGATGGTCATTC 827

RESULT 9
US-09-724-676-20749/c
; Sequence 20749, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20749
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20749

Query Match      100.0%; Score 20; DB 5; Length 1836;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 891 TTTCACCAACGATGGTCATTC 872

RESULT 10
US-09-724-676A-20749/c
; Sequence 20749, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20752
; LENGTH: 3610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20752

Query Match      100.0%; Score 20; DB 5; Length 3610;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 2665 TTTCACCAACGATGGTCATTC 2646

RESULT 11
US-09-724-676-20752/c
; Sequence 20752, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20752
; LENGTH: 3610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20752

Query Match      100.0%; Score 20; DB 5; Length 3610;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 2665 TTTCACCAACGATGGTCATTC 2646

RESULT 12
US-09-724-676A-20752/c
; Sequence 20752, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20752
; LENGTH: 3610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20752

Query Match      100.0%; Score 20; DB 5; Length 3610;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACCAACGATGGTCATTC 20
   |||||
Db 2665 TTTCACCAACGATGGTCATTC 2646

RESULT 13
US-09-724-676-20751/c
```

```

; Sequence 20751, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20751
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20751

```

```

Query Match          100.0%; Score 20; DB 5; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TTTCACCGATGGTCATTC 20
Db 2732 TTTCACCGATGGTCATTC 2713

```

```

RESULT 14
US-09-724-676A-20751/C
; Sequence 20751, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20751
; LENGTH: 3677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-20751

```

```

Query Match          100.0%; Score 20; DB 5; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TTTCACCGATGGTCATTC 20
Db 2732 TTTCACCGATGGTCATTC 2713

```

```

RESULT 15
US-09-724-676-20754/C
; Sequence 20754, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20754
; LENGTH: 3697
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-20754

```

```

Query Match          100.0%; Score 20; DB 5; Length 3697;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TTTCACCGATGGTCATTC 20

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Db 2752 TTTCACCGATGGTCATTC 2733

Search completed: January 12, 2003, 12:07:16
Job time : 170 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: January 12, 2003, 09:41:35 ; Search time 2677 Seconds
(without alignments)
217.429 Million cell updates/sec

Title: US-09-757-100B-18
Perfect score: 20
Sequence: 1 ttccaaccagatggcattc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sta.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
- 35: em_hgt_rod.*
- 36: em_hgt_mam.*
- 37: em_hgt_vrt.*
- 38: em_sy.*
- 39: em_hgtgo_hum.*
- 40: em_hgtgo_mus.*
- 41: em_hgtgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	20	100.0	20	6	AR116330	AR116330 Sequence	
C	2	20	100.0	402	11	G06663	G06663 human STS W
	3	20	100.0	550	6	AX368271	AX368271 Sequence
C	4	20	100.0	3052	9	HUMFAK	L05186 Homo sapien
	5	20	100.0	3199	9	BC028733	BC028733 Homo sapi
C	6	20	100.0	3236	9	AK094999	AK094999 Homo sapi
	7	20	100.0	3791	6	AR116314	AR116314 Sequence
C	8	20	100.0	3791	9	HUMFAKX	L13616 Human focal
	9	20	100.0	4431	9	HSM804272	AL832961 Homo sapi
C	10	20	100.0	4481	6	AX281683	AX281683 Sequence
	11	20	100.0	206467	2	AC067931	AC067931 Homo sapi
C	12	18.4	92.0	3974	1	RME132004	AJ132004 Rhizobium
	13	18.4	92.0	323450	1	SME591790	AL591790 Sinorhizo
C	14	18	90.0	119671	9	AC102801	AC102801 Homo sapi
	15	18	90.0	156235	9	AC084336	AC084336 Homo sapi
C	16	18	90.0	175743	9	AC011632	AC011632 Homo sapi
	17	17.4	87.0	10731	1	AE005765	AE005765 Caulobact
C	18	17.4	87.0	50711	2	AC103694	AC103694 Homo sapi
	19	17.4	87.0	102194	10	AL713916	AL713916 Mouse DNA
C	20	17.4	87.0	113332	2	AC091767	AC091767 Homo sapi
	21	17.4	87.0	150206	8	OSJN00083	AL606668 Oryza sat
C	22	17.4	87.0	155902	9	AP002852	AP002852 Homo sapi
	23	17.4	87.0	182951	2	AC108406	AC108406 Mus muscu
C	24	17.4	87.0	184332	2	AC011777	AC011777 Homo sapi
	25	17.4	87.0	187918	2	AL808135	AL808135 Mus muscu
C	26	17.4	87.0	188895	2	AC106524	AC106524 Rattus no
	27	17.4	87.0	196766	2	AC094333	AC094333 Rattus no
C	28	17.4	87.0	197294	2	AC111560	AC111560 Rattus no
	29	17.4	87.0	200610	9	AP002851	AP002851 Homo sapi
C	30	17.4	87.0	208747	2	AC105614	AC105614 Rattus no
	31	17.4	87.0	246700	2	AL808136	AL808136 Mus muscu
C	32	17.4	87.0	249536	10	AL663072	AL663072 Mouse DNA
	33	17.4	87.0	275548	2	AC098455	AC098455 Rattus no
C	34	17	85.0	1310	8	AB070838	AB070838 Coriolus
	35	17	85.0	78782	2	AC095594	AC095594 Rattus no
C	36	16.8	84.0	1333	4	MEBCASMR	X54715 M.eugenii m
	37	16.8	84.0	1911	6	AX481431	AX481431 Sequence
C	38	16.8	84.0	4465	6	AR007225	AR007225 Sequence
	39	16.8	84.0	4465	6	AR062429	AR062429 Sequence
C	40	16.8	84.0	4465	6	AR170011	AR170011 Sequence
	41	16.8	84.0	4465	6	AR170438	AR170438 Sequence
C	42	16.8	84.0	4465	6	I27715	I27715 Sequence 1
	43	16.8	84.0	4544	6	I06337	I06337 Sequence 20
C	44	16.8	84.0	5427	6	AR036470	AR036470 Sequence
	45	16.8	84.0	5427	6	AR069429	AR069429 Sequence

ALIGNMENTS

RESULT 1
AR116330
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR116330
Sequence 18 from patent US 6133031.
AR116330
AR116330.1 GI:14096652
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Monia, B.P. and Gaarde, W.A.
Antisense inhibition of focal adhesion kinase expression
Patent: US 6133031-A 18 17-OCT-2000;
Location/Qualifiers

20 bp
DNA
linear
PAT 16-MAY-2001

source 1. 20
/organism="unknown"

BASE COUNT 5 a 5 c 3 g 7 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
1 TTTCAACGAGATGTCATTC 20

Db 1 TTTCAACGAGATGTCATTC 20

RESULT 2
G06663 402 bp DNA linear STS 19-OCT-1995
LOCUS human STS WI-7711, sequence tagged site.
ACCESSION G06663
VERSION G06663.1 GI:859908
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STS derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 402)
Hudson.T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)

REFERENCE
AUTHORS Hudson.T.
TITLE Whitehead Institute/MIT Center for Genome Research; Physically
JOURNAL Mapped ESTs
COMMENT

CONTACT: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: GAGCAGCTTGTACCTC
Primer B: AGTTAGGAATTAGATGTACCCC
STS size: 350
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pm
dNTPs: each 4 mM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3

FEATURES
source
1. 402
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="951_H_5; 805.4 CR from top of Chr8 linkage group"

STS
primer_bind 14. 363
primer_bind 14. 33
complement(339..363)
BASE COUNT 117 a 81 c 74 g 111 t 19 others

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 402;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
140 TTTCAACGAGATGTCATTC 121

Db 140 TTTCAACGAGATGTCATTC 121

RESULT 3
AX368271 550 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 981 from Patent WO0204514.
DEFINITION AX368271
ACCESSION AX368271
VERSION AX368271.1 GI:18856344
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1

REFERENCE
AUTHORS Wang, T., Maranabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
Manerakis, M., Carter, D., Fanger, G.R., Vedrick, T.S., Bangur, C.S.,
McNabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.
TITLE Compositions and methods for the therapy and diagnosis of lung
Cancer
JOURNAL Patent: WO 0204514-A 981 17-JAN-2002;
CORIXA CORPORATION (US)

FEATURES
source
1. 550
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 155 a 113 c 121 g 161 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 550;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
195 TTTCAACGAGATGTCATTC 214

Db 195 TTTCAACGAGATGTCATTC 214

RESULT 4
HUMPAK/c 3052 bp mRNA linear PRI 10-JUN-2002
LOCUS Homo sapiens focal adhesion kinase mRNA, complete cds.
DEFINITION L05186
ACCESSION L05186.1 GI:182394
VERSION L05186.1
KEYWORDS focal adhesion kinase; protein-tyrosine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 3052)
REFERENCE
AUTHORS Andre, E. and Becker-Andre, M.
TITLE Expression of an N-terminally truncated form of human focal
adhesion kinase in brain
JOURNAL Biochem. Biophys. Res. Commun. 190 (1), 140-147 (1993)
MEDLINE 93135758
PUBMED 8422239

FEATURES
source
1. 3052
location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cfeature="exon"
/dev_stage="fetal"
15. 2654
/EC_number="2.7.1.1"
/function="protein/tyrosine kinase"


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/codon_start=1
/product="focal adhesion kinase"
/protein_id="AAA35819.1"
/db_xref="GI:182395"
/translation="MSDYVWVGKSNYEVLEKDVGLRFPFKSLSDSVKAKTLRLKLIQ
TQPCANLNRESILKFFELISPVVDFKCEPKCALGSGSWIISVELAIGPEGISYL
TDKGNPTHLADFTQVTOIQVNSDKKGMLOLKIAGAPBLTVAPSLTIAENMA
DLIDGVCRLVNGTSQSFIRPQKEGERALPSIPKLANSKQGNRHVSVSETDDYAE
IIDEEDTYTMSPTREDYEIQERIELGRCIGEGQFQDVHOGIYMSNPENPALVAIKTK
NCTSDVRKFLQEAHYTSLHNWCRIYSDPNVDAPDPNRAELTMRFQDHPHIVKL
IGVITENPVMIIMELCTLGLRSLFVQRYKSLDLSLILYAYQLSTALAYLESKRFVH
IDTAARVLVNSNDCKLGDGLSLRYMEDSTYVYKASKGLPIKMAPEINRRTFTA
SDVWVGVCWMLHGVKPGQVKNNDVIGRIENGERLPMPCNPCTIYLSMTKCA
YDPSRRPTELEKQSLTILEEKAQOERMESRRQATVSWDSGDEAPPKFSRP
GSPSRSSSGFVPSPOHMQTNHYQVSGPGSHGITAMAGSIYPGASLDDDTSNWH
RQOEIAMWQNVEDSTLRLGQVLPHTLMELRIQOQMEEDQRLWEERFLI
GNOHIYQVGVKDPAAKPPKPPGAPAGHLGSLASLSSPADSYNEGVKLQPOEISPPP
TANLDRSNKVYENVTLGVKAVIEMSSKIQAPPEYVPMVKEVGLALRTLATVDET
IPLLPASTHREIEMAQKLNSDLGELINKMKAQYVMTSLQOEYKKQMLTAHALAV
DAKNLLDVIDQARKMLGQTRPH"
BASE COUNT      910 a  680 c  724 g  738 t
ORIGIN
      1 TTTCAACACAGATGGTCATTC 20
      |||||
      2792 TTTCAACACAGATGGTCATTC 2773

Query Match      100.0%; Score 20; DB 9; Length 3052;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAACACAGATGGTCATTC 20
    |||||
    2792 TTTCAACACAGATGGTCATTC 2773

RESULT 5
BC028733/c
LOCUS
DEFINITION
Homo sapiens, Similar to PTK2 protein tyrosine kinase 2, clone
MGC:33483 IMAGE:4812915, mRNA, complete cds.
ACCESSION
BC028733
VERSION
BC028733.1 GI:22382093
KEYWORDS
MGC.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3199)
Strausberg,R.
Direct Submission
Submitted (29-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Niklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrived by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 46 Row: d Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency Orf
analysis.
Location/Qualifiers
1..3199
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="MGC:33483 IMAGE:4812915"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"
80..2122
/codon_start=1
/product="Similar to PTK2 protein tyrosine kinase 2"
/protein_id="AAH28733.1"
/db_xref="GI:22382094"
/translation="MKYQEVCLTSFNISVSPFAETDDYAEIIDEEDTYTMSPTDYE
IQERIELGRCIGEGQFQDVHOGIYMSNPENPALVAIKTCNCTSDSVREPLEQALIT
MRQDPHPIVLLIGVITENPVMIIMELCTLGLRSLFVQRYKSLDLSLILYAYQLST
ALAYLESKRFVHIGVKNNDVIGRIENGERLPMPCNPCTIYLSMTKCA
YDPSRRPTELEKQSLTILEEKAQOERMESRRQATVSWDSGDEAPPKFSRP
GSPSRSSSGFVPSPOHMQTNHYQVSGPGSHGITAMAGSIYPGASLDDDTSNWH
RQOEIAMWQNVEDSTLRLGQVLPHTLMELRIQOQMEEDQRLWEERFLI
GNOHIYQVGVKDPAAKPPKPPGAPAGHLGSLASLSSPADSYNEGVKLQPOEISPPP
TANLDRSNKVYENVTLGVKAVIEMSSKIQAPPEYVPMVKEVGLALRTLATVDET
IPLLPASTHREIEMAQKLNSDLGELINKMKAQYVMTSLQOEYKKQMLTAHALAVDAKNLLDVIDQARKMLGQTRRH"
BASE COUNT      956 a  676 c  718 g  849 t
ORIGIN
      1 TTTCAACACAGATGGTCATTC 20
      |||||
      2260 TTTCAACACAGATGGTCATTC 2241

Query Match      100.0%; Score 20; DB 9; Length 3199;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCAACACAGATGGTCATTC 20
    |||||
    2260 TTTCAACACAGATGGTCATTC 2241

RESULT 6
AK094999/c
LOCUS
DEFINITION
Homo sapiens cdna FLJ37680 fis, clone BRHIP2012923, highly similar
to FOCAL ADHESION KINASE 1 (EC 2.7.1.112).
ACCESSION
AK094999
VERSION
AK094999.1 GI:21754175
KEYWORDS
Homo sapiens hippocampus cdna to mRNA, clone BRHIP2
clone:BRHIP2012923.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cdna sequencing project
Unpublished
2 (bases 1 to 3236)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cdna sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cdna full insert sequencing:
Research Association for Biotechnology (RAB); cdna library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and

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RAB; annotation: HRI and RAB.
FEATURES
source location/Qualifiers
1..3236 /organism="Homo sapiens"
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/clone="BRHIP2012923"
/tissue_type="hippocampus"
/clone_lib="BRHIP2"
/note="cloning vector: pME18FL3"
13..2175 /note="unnamed protein product"
/codon_start=1
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/db_xref="GI:21754176"
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NPVWIMELCTGELRSFLQVRYKSLDASLILVAYQSTALAYLESKRFVRIIDAR
NVLVSNDVCVLGDFGLSRVMDSTYYKASKKLPIKMAPEISINFRFSTASDVMMF
GYCMWEILMHGKYPQGVKNNVIRIENGRELPMPCPPTLYSLMTKMAYPDSSR
PREFLKAKQSTILLEEKAOQDERKRMESRQATVSMDSGSDAPPRKSPGTPSPR
SSEGFYSPQHWQTNHYQVSGYPSHGITYMAGSIYEQASLLDQTSWMHPELIA
MMQPNVEDSTVLDRIGIQVLPHTLMESRLIROQEMEDQRMLEKERFLKPDVRLS
RGSIDREDSLOGPIGNOHIVQVGPDPAPPKPPRGAHGLSLASISPADSY
NEGVLQPOEISPPPTANLDRSNDKVENVTGLVAVIEMSKIQPAPPEEYVPMVKE
VGLARTILATYDERTPLLPASTHEIEMACQLNSDGLINKKLAQOYVMTSLQ
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BASE COUNT 961 a 697 c 741 g 837 t
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCAACGAGATGTCATTC 20
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Db 2313 TTTCAACGAGATGTCATTC 2294
RESULT 7
LOCUS AR116314 3791 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6133031.
ACCESSION AR116314
VERSION AR116314.1 GI:14096636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3791)
AUTHORS Monta, B.P. and Gaarde, W.A.
TITLE Antisense inhibition of focal adhesion kinase expression
JOURNAL Patent: US 6133031-A 1 17-OCT-2000;
FEATURES location/Qualifiers
source 1..3791 /organism="unknown"
BASE COUNT 1110 a 849 c 924 g 908 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3791;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCAACGAGATGTCATTC 20
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Db 3529 TTTCAACGAGATGTCATTC 3510
RESULT 8
LOCUS HUMPAKX/c 3791 bp mRNA linear PRI 31-DEC-1994
DEFINITION Human focal adhesion kinase (FAK) mRNA, complete cds.
ACCESSION L13616

VERSION L13616.1 GI:439874
KEYWORDS focal adhesion kinase; tyrosine kinase.
SOURCE Homo sapiens (tissue library: lambda fcl1) T-lymphocyte cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3791)
AUTHORS Whitney, G.S., Chan, P.Y., Blake, J., Cosand, W.L., Neubauer, M.G.,
Aruffo, A. and Kanner, S.B.
TITLE Human T and B lymphocytes express a structurally conserved focal
JOURNAL adhesion kinase, pp125FAK
MEDLINE DNA Cell Biol. 12 (9), 823-830 (1993)
PIRMEID 7692878
COMMENT 7692878
FEATURES
source location/Qualifiers
1..3791 /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="T-lymphocyte"
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1..232 /gene="FAK"
/note="putative"
233..3391 /gene="FAK"
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GVSREKVELAPPEEKYELRIYRYPGFLNOFDEKDTLPNFPYQVSSDMLLEIA
DOUOEIALKGLCEIETRSYWMENGNALKEKSYEULEKVGKLRPFKSLDSYKAK
TURKLIQOTFRPANNLNRBSILKFFETLSVTRFDEKCFKALGSSWIIISVELAIGP
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TIAENMADLIDGYCRLVNGTSGSFIIRPOKEGRALPSIPKLANSEKGRTHAVSVS
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VAITCKNCTSDVREKFLQEAULTMOPHPHIVKLIQVITENPWTIMELCTGELRS
FLQVRYKSYSLDASLILVAYQSTALAYLESKRFVRIIDARNVLSNDVCVLGDFGLSR
VLMEDSTYYKASKKLPIKMAPEISINFRFTSADVMMFGYCMWEILMHGKYPQ
GKNNADVIGRIENGERLPMPCPPTLYSLMTKMAYPDSSRPFELKAKQSTILLEE
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HYQVSGYPSHGITYMAGSIYEQASLLDQTSWMHPELIRIOMQPNVEDSTVLDRIG
IGQVLPHTLMESRLIROQEMEDQRMLEKERFLKPDVRLSIRGSDREDSLOGP
NOHTYQVGPDPAPPKPPRGAHGLSLASISPADSYNEGVLQPOEISPPPTANLDRS
NDKVENVTGLVAVIEMSKIQPAPPEEYVPMVKEVGLARTILATYDERTPLLPASTH
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3' UTR
BASE COUNT 1110 a 849 c 924 g 908 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 3791;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCAACGAGATGTCATTC 20
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Db 3529 TTTCAACGAGATGTCATTC 3510
RESULT 9
LOCUS HSM804272 4431 bp mRNA linear PRI 10-JUL-2002
DEFINITION Homo sapiens mRNA; cDNA DKFZp66600110 (from clone DKFZp66600110).
ACCESSION AL632961
VERSION AL632961.1 GI:21733549

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KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4431)
AUTHORS
Ansoerge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUL-2002) 1, D-85764 Neuberberg, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp66600110) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/clone_lib="666 (synonym: hsto2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev stage="adult"
polya signal
4383..4388
polya_site
4399
BASE COUNT
1325 a 959 c 1023 g 1124 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 4431;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAACACGATGTCATTC 20
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Db 3479 TTCAACACGATGTCATTC 3460
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RESULT 10
AX281683/c
LOCUS
DEFINITION
Sequence 92 from Patent WO0177389.
ACCESSION
AX281683
VERSION
AX281683.1 GI:16608934
KEYWORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
Mikita,T. and Tai,J.
TITLE
Genes expressed in foam cell differentiation
JOURNAL
Patent: WO 0177389-A 92 18-OCT-2001;
Incyte Genomics, Inc. (US)
FEATURES
Location/Qualifiers
source
1..4481
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/db xref="taxon:9606"
/notes="Incyte ID No: 242114.16"
BASE COUNT
1326 a 974 c 1045 g 1136 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3558 TTCAACACGATGTCATTC 3539
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RESULT 11
AC067931
LOCUS
DEFINITION
Homo sapiens chromosome 8 clone RP11-642A1 map 8, *** SEQUENCING IN
PROGRESS ***, 1 ordered piece.
ACCESSION
AC067931
VERSION
AC067931.15 GI:22122968
KEYWORDS
HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 206467)
AUTHORS
Birren,B., Nusbaum,C. and Lander,E.
TITLE
Homo sapiens chromosome 8, clone RP11-642A1
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 206467)
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choquel,Y., Colangelo,M., Collins,S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Lander,S., Lehotzky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,N.,
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Navlor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivat,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 206467)
AUTHORS
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choquel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Navlor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,K., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 6, 2002 this sequence version replaced gi:21450497.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

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Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10082
Center clone name: 642_A_1

* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 206467: contig of 206467 bp in length.
Location/Qualifiers
1. 206467
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/db_xref="taxon:9606"
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/clone="RP11-642A1"
/clone_lib="RPC1-11 Human Male BAC"
BASE COUNT 57619 a 50155 c 48369 g 50320 t 4 others
ORIGIN
Query Match 100.0%; Score 20; DB 2; Length 206467;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCACCGAGATGTCATTTC 20
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Db 135959 TTTCACCGAGATGTCATTTC 135978
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RESULT 12
RMEI32004 3974 bp DNA linear BCT 25-MAR-1999
LOCUS Rhizobium melioli c1p and leuA genes, ORF83 and ORF142.
DEFINITION
ACCESSION AJ132004
VERSION AJ132004.1 GI:4539548
KEYWORDS 2-isopropylmalate synthase; c1p protease; c1p gene; leuA gene;
leucine biosynthesis; ORF142; ORF83; proteolytic subunit.
SOURCE Sinorhizobium melioli.
ORGANISM Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 3974)
Sanjuan-Pinilla,J.M., Olivares,J. and Sanjuan,J.
The Rhizobium melioli leuA gene is essential for symbiosis
Unpublished
2 (bases 1 to 3974)
Sanjuan,J.
Direct Submission
Submitted (24-FEB-1999) Sanjuan J., Microbiologia del Suelo y
Sistemas Simbioticos, Estacion Experimental del Zaidin-CSIC,
Profesor Albarada 1, E-18008 Granada, SPAIN
FEATURES
source
1.3974
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/protein_id="CAB39976.1"
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/translation="MRNDQDEKTEPLPGKETANLFKRSITFYGTITQELAQXV

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ADTAAKMITDMAAKAGGGRFEYSPEEFTELEVALEICNAVEIYRPPADNGLIN
LPSTVENATPNIYADQIEMMCRLNDRENIIVSIAPHNDGSGIAATDGLMAGADRV
EGTLFNGERTGNVDVVTLLNMTQGVDPKLDSDIERIKEYEYSGRYEAMIRINSOS
GKGIVYTAFGSGHDAINKGMKAIKQANKTPWEPYPIPIPDVGRSVEAMIRINSOS
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/protein_id="CAB39978.1"
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3289..3717
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/db_xref="GI:4539552"
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AALTRLRLIATKGRADRSIDLGEARELVDSEFIQALSASEVTIDSHSTGRALDAMARVG
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BASE COUNT 828 a 1198 c 1205 g 743 t
ORIGIN
Query Match 92.0%; Score 18.4; DB 1; Length 3974;
Best Local Similarity 95.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 TTTCACCGAGATGTCATTTC 20
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Db 2159 TTTCACCGAGATGTCATTTC 2178
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RESULT 13
SMES591790/c 323450 bp DNA linear BCT 05-JUL-2002
LOCUS Sinorhizobium melioli 1021 complete chromosome; segment 9/12.
DEFINITION
ACCESSION AL591790 AL591688
VERSION AL591790.1 GI:15075230
KEYWORDS
SOURCE Sinorhizobium melioli.
ORGANISM Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 323450)
Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batur,J.,
Boistard,P., Becker,A., Bouty,M., Cadieu,B., Dreano,S., Gloux,S.,
Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Maauy,D.,
Pohl,T., Portetalle,D., Puhler,A., Purnelle,B., Ramsperger,U.,
Renard,C., Thebaud,P., Vandenbol,M., Weidner,S. and Galibert,F.
Analysis of the chromosome sequence of the legume symbiont

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	Sinorhizobium meliloti strain 1021 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9877-9882 (2001) 21396507 11481430 2 (bases 1 to 323450) Gouzy, J. Direct Submission Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO EU Consortium	gene CDS	KAHLSGAEGETCALLDRRAGTIQPLAYARGLARAAAGAEIFTDTPLLAASRGDDL WNLKTPRGTVTARHVLATNAYGSLVTGVPWKEYROELTILPYFOFATNPLPDNVAAR ILPERGAWDITGLVMTSPMRDQNRLLIFGSIQGLDAIAAGTHRAFAARSVKLPFYIG DFRFEHWDGRIGMTTNNLPAHVLAPNVVISGNGYAGIAPGTVFGRALARHVTGDT SAIPLAETPVTDPWPRTLKSAFVHAGAQAQKHFIDKRF" complement (3024..3740) /gene="SMC01579" complement (3024..3740) /gene="SMC01579" /function="miscellaneous; hypothetical/global homology" /note="Product confidence : hypothetical Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD" /codon_start=1 /evidence=not experimental /transl_table=11 /product="CONSERVED HYPOTHETICAL PROTEIN" /protein_id="CAC46789.1" /db_xref="GI:15075233" /db_xref="SPTREMBL:Q92NJ2" /translation="MAVITFANAKGAGKTTAALILSTELARQGNVVVLDADPORWI TSMSEVSRVANLEVISHTVPASLPHCHIRELGEADFVIDLAGAKDAIVALALGSLD HVLIPVQCANDARGAVQILELIRHIGEKARVRINHVSVLTRVNSLVTTRALQTIKAL LASRGVSLDTPIVERVAYREIFECCGTLQMMDPNRVSNLKDARENAVAAAEVQNL PVTARRALMSRLRSALPRAA" complement (3949..5094) /gene="SMC01582" complement (3949..5094) /gene="SMC01582" /EC_number="1.1.1.-" /function="small molecule metabolism" /note="Product confidence : putative Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD" /codon_start=1 /evidence=not experimental /transl_table=11 /product="PUTATIVE ALCOHOL DEHYDROGENASE PROTEIN" /protein_id="CAC46790.1" /db_xref="GI:15075234" /db_xref="SPTREMBL:Q92NJI" /translation="MTITANWSYPTAVKFGAGRIKELADHCKALGKKPLLVTRDGLA PMATQQALDILEAGLGRAIFADVDPNPNDRNLEAGVKASRDGDGCVAFGGSGGL DLKCVAFMAQGTFRVWDFEIDGWWTRASVEGIIAPIVAVPTTAGTSGEVGRASVITN SASHVKVIFHFPLPGVTICDPELTVMGPVKVITAGTMDAFAPHCLEAYSGSPFHPMS AGIALGEMRLVKYLPKADGADLEARNKMMVMAAMGAVAFQKGLGAIHSLSHFVGA IYNTHHGMTNAVMPVPLNRSALIEEKIGRAAAAYLIGAGFDGFDYDVLRLREELGV PKLSALGVGTDRIDEMAEMAIVDPTAGNPNVELTDLAAEKLFAECI" complement (5091..6476) /gene="SMC01588" complement (5091..6476) /gene="SMC01588" /EC_number="1.2.1.-" /function="small molecule metabolism" /note="Product confidence : putative Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD" /codon_start=1 /evidence=not experimental /transl_table=11 /product="PUTATIVE ALDEHYDE DEHYDROGENASE PROTEIN" /protein_id="CAC46791.1" /db_xref="GI:15075235" /db_xref="SPTREMBL:Q92NJO" /translation="WTMIRCVSPDGEVYASERPAIPLEMAQVAHARLAOKAWARRP LDREVKVLAVAGRLNMEVDVPELAWMGPRVRYGGEFGFNGERSNYASIALADAL KPLVVEESDRFERRIAREPHGVFVFIAPWNPYPTAINTVAPMAGNTVILKHASOT
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL	MELILO EU Consortium: Laboratoire de Biologie Molculaire des Relations Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet, France, Laboratoire de Genetique et Developpement UMR6061-CNRS, Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes, France, GARC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany, Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25, D-33615 Bielefeld, Germany, Unite de Biochimie Physiologique, Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20, 1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6, B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@coulouse.inra.fr http://sequence.toulouse.inra.fr/meliloti.html. Location/Qualifiers 1..323450 /organism="Sinorhizobium meliloti" /strain="1021" /db_xref="taxon:382" 155..1519 /gene="SMC01575" 155..1519 /gene="SMC01575" /function="miscellaneous; hypothetical/partial homology" /note="Product confidence : hypothetical Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD" /codon_start=1 /evidence=not experimental /transl_table=11 /product="HYPOTHETICAL PROTEIN" /protein_id="CAC46787.1" /db_xref="GI:15075231" /db_xref="SPTREMBL:Q92K34" /translation="MTPATRTGLSLFAALALMAMELAPANAQDAYGGYGGGVMLVT PEGDILDYIPGEAEHAMDRGRITVLDPWGNIVATVVPNDYGRGRRYGRDGY PEPRDRGYGSPGEFTGAIPEVRDIAPAPEREDLPNSLPSLSDREBAAYDPOYDDP LAQMPMPAMTVTKGSAEIAALQVFLDRGSPGVIDGKWSNVTKAIEAWQAQGTET LDPNNTEDILRLRNFNGGLPITYITITADAAGFPVASIPEDTAHKAQLPHLSFTSVT EMLGEKPHDEAYLRELNFGVDPSIPGTTIKVNPNGNKKGVARIADKARKQVLA DEAGKLIAAPSTIGSSDTPSPSGTVHVERIAFPDGYTYNPKINFQOGANDRIILQIQ GNPGPVGTWVIALSKPTYGIHGTPEPSKIGTKQSHGCVRLTNWDATELGKMYSTGTVV EFVD" 1707..2996 /gene="SMC01576" 1707..2996 /gene="SMC01576" /function="small molecule metabolism" /note="Product confidence : putative Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD" /codon_start=1 /evidence=not experimental /transl_table=11 /product="PUTATIVE OXIDOREDUCTASE PROTEIN" /protein_id="CAC46788.1" /db_xref="GI:15075232" /db_xref="SPTREMBL:Q92NJ3" /translation="WATERALPNLWHTAPAPRTAPLAGDLTVEVAIVCGGFTGLSA ALHIAETGRTAVIEARMIGFGSGNRNVLNAGMWVQPDIDTIATIGAGAKNRLLDEL GGGPFVYDLVAKHGIECEAVRNGTLHMSVGAEGLKEITREREQWKKGAPVEVLSAE	gene CDS	

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AC102801
VERSION AC102801.2 GI:20377028
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SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 119671)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Browman,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dode,S., Fato,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Grinde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heard,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
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McCarthy,M., McEwan,P., McKernan,K., McPheters,R., Meldrim,J.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunhphang,P., Pierre,N., Pollard,V.,
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Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02144, USA
3 (bases 1 to 119671)
REFERENCE
JOURNAL TITLE
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dode,S.,
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Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
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Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-MAY-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02144, USA
On May 1, 2002 this sequence version replaced gi:117060911.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L19703
Center clone name: 960_P_16
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SP6 end overlaps project AC011632 (L2781) by 63.5 kilobases; T7 end
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 156235)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 156235)
AUTHORS
Anderson,S., Barna,N., Bastien,V., Bada,F., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepl,Y., Collangeio,M., Collins,S., Collymore,A., Cooke,P.,
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Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
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Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (25-OCT-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 156235)
REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhvalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 156235)
REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhvalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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Maclean, C., Macdonald, P., Major, J., Margis, N., Matthews, C.,
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Meneus, L., Mihova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnpbach, R.,
Seaman, S., Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 11, 2001 this sequence version replaced gi:15042917.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

COMMENT ----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LI0933
Center clone name: 625_F_15
----- Location/Qualifiers

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 2185239 seqs, 1125999159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAC65550	Human focal adhesi
2	20	100.0	20	AAS15398	Human focal adhesi
3	20	100.0	550	ABK38943	cDNA encoding lung
c 4	20	100.0	3791	22 AAC65534	Human focal adhesi
c 5	20	100.0	3791	24 AAS15382	Human focal adhesi
c 6	20	100.0	4052	23 ABV29192	Human prostate exp
c 7	20	100.0	4481	24 AAS94837	Human DNA sequence
c 8	18.4	92.0	707	22 AA197828	Human neuroblastom
9	17	85.0	1311	24 ABA93211	Coriolus versicolor

10	16.8	84.0	244	22	ABA51579	Human breast cell
11	16.8	84.0	244	22	ABA35555	Probe #15021 for g
12	16.8	84.0	244	22	AAK43716	Human bone marrow
13	16.8	84.0	400	22	ABA46482	Human breast cell
14	16.8	84.0	400	22	ABA26688	Probe #5154 for ge
15	16.8	84.0	400	22	AAK30708	Human bone marrow
16	16.8	84.0	528	22	AAK37562	Human bone marrow
17	16.8	84.0	528	22	AAI43434	Probe #12120 used
18	16.8	84.0	1681	14	AAQ34687	Babesia equi subcl
c 19	16.8	84.0	1911	24	ABL91702	Human polynucleoti
c 20	16.8	84.0	4544	10	AAAN90355	cDNA encoding plat
c 21	16.8	84.0	4544	17	AAAT34552	platelet-derived g
c 22	16.8	84.0	5427	13	AAQ27447	Type B human plate
c 23	16.8	84.0	5602	23	AAAS84940	cDNA encoding novel
c 24	16.8	84.0	5719	10	AAAN90388	cDNA encoding huma
c 25	16.8	84.0	6390	23	AAAS79665	DNA encoding novel
c 26	16.8	84.0	6390	23	AAAS84936	DNA encoding novel
c 27	16.8	84.0	11036	20	AAAX13401	Enterococcus faeca
c 28	16.8	84.0	32191	22	AAAS26704	Human genomic DNA
c 29	16.8	84.0	49561	22	AAK82012	Human immune/haema
30	16.4	82.0	4094	21	AAZ51205	Human hypoxia regu
31	15.8	79.0	175	21	AAAC14051	Human secreted pro
32	15.8	79.0	476	24	ABL83730	Human ovarian canc
33	15.8	79.0	490	23	AAAS87979	DNA encoding novel
34	15.8	79.0	575	24	ABK78062	Bacillus clausii g
35	15.8	79.0	579	23	AAAS68415	DNA encoding novel
c 36	15.8	79.0	709	18	AAAX30750	Streptococcus pneu
c 37	15.8	79.0	822	23	AAAS7983	DNA encoding novel
c 38	15.8	79.0	860	21	AAA05546	Streptococcus pneu
c 39	15.8	79.0	1020	23	AAAS55500	Streptococcus pneu
c 40	15.8	79.0	1020	23	AAAS5900	Streptococcus pneu
41	15.8	79.0	1377	24	AAAS2851	Yersinia pseudotub
42	15.8	79.0	2286	23	AAAS92528	DNA encoding novel
c 43	15.8	79.0	3643	23	ABL03334	Drosophila melanog
44	15.8	79.0	5304	23	ABL20423	Drosophila melanog
45	15.8	79.0	5358	23	ABL04503	Drosophila melanog

ALIGNMENTS

RESULT 1

AAC65550

ID AAC65550 standard; DNA; 20 BP.

XX

AC AAC65550;

XX

DT 12-FEB-2001 (first entry)

XX

DE Human focal adhesion kinase antisense sequence #16.

XX

KW Human; focal adhesion kinase; FAK; signal transduction; cancer;

KW embryonic development disorder; angiogenic disorder; wound healing;

KW antisense; phosphorothioate; ss.

XX

OS Homo sapiens.

XX

PN US6133031-A.

XX

PD 17-OCT-2000.

XX

PF 19-AUG-1999; 99US-0377310.

XX

PR 19-AUG-1999; 99US-0377310.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Monia BP, Gaarde WA;

XX

DR WPI; 2001-006141/01.

XX

PT New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal

PT neovascularization, or for diagnosing and treating e.g. colon cancer -
 XX
 PS Claim 3; Column 23; 30pp; English.
 XX
 CC The present invention describes a number of phosphorothioate antisense
 CC sequences to the human focal adhesion kinase (FAK) protein. This protein
 CC is involved in integrin-mediated signal transduction, and is implicated
 CC in cancer, particularly colon, breast and oral tumours, embryonic
 CC development disorders, angiogenic disorders and wound healing. The
 CC antisense sequences, including the one shown here, can be used in the
 CC treatment of all of these.
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 SQ Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;
 Query Match 100.0%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 TTTCACCGAGTGCATTC 20
 RESULT 2
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 ID AAS15398 standard; DNA; 20 BP.
 XX
 AC AAS15398;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human focal adhesion kinase (FAK) antisense oligonucleotide IS1515421.
 XX
 KW Human; focal adhesion kinase; FAK; melanoma; tumour metastasis;
 KW cancer; angiogenic disorder; retinal neovascularisation; cytosolic;
 KW ophthalmological; antisense; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate internucleotide linkages,
 optional bases 1-5 and 16-20 are
 2'-methoxyethoxy (2'-MOE) bases, where the
 2'-MOE cytosines are also 5'-methylcytosines"
 XX
 PN US2001034329-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 09-JAN-2001; 2001US-0757100.
 XX
 PR 19-AUG-1999; 99US-0377310.
 PR 13-JUL-2000; 2000WO-US18999.
 XX
 PA (MONI/) MONIA B P.
 PA (GAAR/) GAARDE W A.
 PA (NERO/) NERO P S.
 XX
 PI Monia BP, Gaarde WA, Nero PS;
 XX
 DR WPI; 2002-010103/01.
 XX
 PT Antisense suppression of Focal Adhesion Kinase expression for the
 PT treatment of cancers of the breast, colon, mouth or skin (especially a
 PT melanoma), and angiogenic disorders e.g. retinal neovascularisation -
 XX
 PS Claim 3; Page 12; 19pp; English.
 XX
 CC The present invention relates to novel antisense compounds which can be
 CC used for modulating the expression of human focal adhesion kinase (FAK).

CC The antisense compounds comprise antisense oligonucleotides
 CC (8-30 nucleotides in length) targeted to the 5'-untranslated region,
 CC translational termination region or 3'-untranslated region of a nucleic
 CC acid molecule encoding FAK. The antisense oligonucleotides can be used
 CC to inhibit the expression of FAK mRNA. The antisense oligonucleotides
 CC represent potential chemotherapeutic agents in the treatment of melanoma
 CC and the prevention of tumour metastasis. The antisense compounds and
 CC method are useful for treating diseases associated with overexpression
 CC or constitutive activation of FAK. Such diseases include cancers of the
 CC breast, colon, mouth or skin (especially a melanoma), and angiogenic
 CC disorders such as retinal neovascularisation. AAS15383-AAS15422
 CC represent the FAK antisense oligonucleotides of the invention.
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 3 G; 7 T; 0 other;
 Query Match 100.0%; Score 20; DB 24; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.78;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTCACCGAGTGCATTC 20
 DB 1 TTTCACCGAGTGCATTC 20
 RESULT 3
 ABK38943
 ID ABK38943 standard; cDNA; 550 BP.
 XX
 AC ABK38943;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE cDNA encoding lung tumour protein clone R0127.G07.
 XX
 KW Lung tumour; cancer; T cell; immune response stimulator;
 KW cytosolic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200204514-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 10-JUL-2001; 2001WO-US22058.
 XX
 PR 11-JUL-2000; 2000US-0614124.
 PR 29-AUG-2000; 2000US-0651563.
 PR 08-SEP-2000; 2000US-0658824.
 PR 26-SEP-2000; 2000US-0671335.
 PR 06-OCT-2000; 2000US-0677419.
 PR 30-OCT-2000; 2000US-0702705.
 PR 13-DEC-2000; 2000US-0736457.
 PR 03-MAY-2001; 2001US-0849626.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW,
 PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
 PI McNabb A, Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
 XX
 DR WPI; 2002-164634/21.
 XX
 PT Novel polynucleotide encoding a lung tumour polypeptide useful for
 PT stimulating and/or expanding T cells specific for a tumour protein -
 XX
 PS Claim 1; SEQ ID No 981; 223pp; English.
 XX
 CC The invention describes an isolated polynucleotide and polypeptide
 CC useful for stimulating and/or expanding T cells specific for a tumour
 CC protein for determining the presence of a cancer in a patient. A
 CC composition containing the polynucleotide and/or polypeptide is useful
 CC for treating a lung cancer in a patient. The polypeptide is useful for
 CC removing tumour cells from a biological sample. The polynucleotide is

CC also useful as probe or primer to detect the level of mRNA encoding a
CC tumour protein. This sequence encodes a lung tumour associated protein
CC or protein fragment, described in the method of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CX
SQ Sequence 550 BP; 155 A; 113 C; 121 G; 161 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACAGATGGTCATTC 20
DB 195 TTTCACACAGATGGTCATTC 214

RESULT 4
AAC65534/c
ID AAC65534 standard; DNA; 3791 BP.
AC
AC AAC65534;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human focal adhesion kinase coding sequence.
XX
DE Human; focal adhesion kinase; FAK; signal transduction; cancer;
KW embryonic development disorder; angiogenic disorder; wound healing; ds.
KW
XX Homo sapiens.
OS
XX
PN US6133031-A.
XX
PD 17-OCT-2000.
XX
PF 19-AUG-1999; 99US-0377310.
XX
PR 19-AUG-1999; 99US-0377310.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Gaarde WA;
XX P-PSDB; AAB30327.
DR
XX
XX New antisense compounds for inhibiting focal adhesion kinase
PT expression, especially useful for inhibiting retinal
PT neovascularization, or for diagnosing and treating e.g. colon cancer -
XX
XX Claim 1; Column 31-40; 30pp; English.
XX
CC The present invention describes a number of phosphorothioate antisense
CC sequences to the human focal adhesion kinase (FAK) protein. This protein
CC is involved in integrin-mediated signal transduction, and is implicated
CC in cancer, particularly colon, breast and oral tumours, embryonic
CC development disorders, angiogenic disorders and wound healing. The
CC antisense sequences can be used in the treatment of all of these.
XX
SQ Sequence 3791 BP; 1110 A; 849 C; 924 G; 908 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3791;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACAGATGGTCATTC 20
DB 3529 TTTCACACAGATGGTCATTC 3510

RESULT 6
ABV29192/c
ID ABV29192 standard; cDNA; 4052 BP.
XX

RESULT 5
AAS15382/c
ID AAS15382 standard; cDNA; 3791 BP.
XX
AC AAS15382;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human focal adhesion kinase (FAK) cDNA sequence.
XX
KW Human; focal adhesion kinase; FAK; melanoma; tumour metastasis;
KW cancer; angiogenic disorder; retinal neovascularisation; cytostatic;
KW ophthalmological; ss.
XX
OS Homo sapiens.
XX
PN US2001034329-A1.
XX
PD 25-OCT-2001.
XX
PF 09-JAN-2001; 2001US-0757100.
XX
PR 19-AUG-1999; 99US-0377310.
PR 13-JUL-2000; 2000WO-US18999.
XX
XX (MONI/) MONIA B P.
PA (GAAR/) GAARDE W A.
PA (NERO/) NERO P S.
XX
PI Monia BP, Gaarde WA, Nero PS;
XX
XX WPI; 2002-010103/01.
DR
XX
XX Antisense suppression of Focal Adhesion Kinase expression for the
PT treatment of cancers of the breast, colon, mouth or skin (especially a
PT melanoma), and angiogenic disorders e.g. retinal neovascularisation -
XX
XX Example 2; Page -; 19pp; English.
XX
CC The present invention relates to novel antisense compounds which can be
CC used for modulating the expression of human focal adhesion kinase (FAK).
CC The antisense compounds comprise antisense oligonucleotides
CC (8-30 nucleotides in length) targeted to the 5'-untranslated region,
CC translational termination region or 3' untranslated region of a nucleic
CC acid molecule encoding FAK. The antisense oligonucleotides can be used
CC to inhibit the expression of FAK mRNA. The antisense oligonucleotides
CC represent potential chemotherapeutic agents in the treatment of melanoma
CC and the prevention of tumour metastasis. The antisense compounds and
CC methods are useful for treating diseases associated with overexpression
CC or constitutive activation of FAK. Such diseases include cancers of the
CC breast, colon, mouth or skin (especially a melanoma), and angiogenic
CC disorders such as retinal neovascularisation. The present cDNA sequence
CC for human FAK is used to design the FAK antisense oligonucleotides
CC of the invention.
CC Note: This sequence (Genbank accession number U13616) is not given in
CC the patent but is acquired by the indexer from Genbank from the
CC information provided in the patent.
XX
SQ Sequence 3791 BP; 1110 A; 849 C; 924 G; 908 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3791;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCACACAGATGGTCATTC 20
DB 3529 TTTCACACAGATGGTCATTC 3510

RESULT 6
ABV29192/c
ID ABV29192 standard; cDNA; 4052 BP.
XX

AC ABV29192;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker CDNA 29183.
DE
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
KM
XX Homo sapiens.
OS
XX WO200160860-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US05171.
PF
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189662P.
XX 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
XX 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
PI
XX
XX WPI; 2001-662795/76.
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer. useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
PS
XX Claim 1; Page 6216-6217; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 4052 BP; 1199 A; 906 C; 971 G; 970 T; 6 other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 23; Length 4052;
XX Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 3536 TTTCACGAGATGTCATTTC 3517

RESULT 7
AAS94837/C
ID AAS94837 standard; DNA; 4481 BP.
XX
XX AAS94837;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Human DNA sequence #92 expressed during foam cell differentiation.
DE
XX

KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX WO200177389-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 04-APR-2001; 2001WO-US11128.
PF
XX
XX 05-APR-2000; 2000US-195106P.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter GJ, Mikita T,
PI Tai J;
PI
XX
XX WPI; 2002-010925/01.
DR
XX
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development -
PS
XX Claim 1; Page 145-146; 315pp; English.
XX
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used
CC as PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation.
XX
XX Sequence 4481 BP; 1326 A; 974 C; 1045 G; 1136 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 24; Length 4481;
XX Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCACGAGATGTCATTTC 20
DB 3558 TTTCACGAGATGTCATTTC 3539

RESULT 8
AA197828
ID AA197828 standard; CDNA; 707 BP.
XX
XX AA197828;
AC
XX
XX 13-NOV-2001 (first entry)
DT
XX
XX Human neuroblastoma expressed polynucleotide SEQ ID NO 3903.
DE
XX
XX Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
KW
XX Homo sapiens.
OS
XX WO200166719-A1.
PN
XX
XX 13-SEP-2001.
PD
XX
XX 02-MAR-2001; 2001WO-JP01629.
PF
XX
XX 07-MAR-2000; 2000JP-0159195.
PR
XX
XX

PA (CHIB-) CHIBA PREPECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 XX Nakagawara A;
 XX WPI; 2001-565584/63.
 XX
 XX Nucleic acids originating in gene expressed in human neuroblastoma,
 PT useful as probe or primer in diagnosing prognosis of human
 PT neuroblastoma, malignancy and susceptibility indicator or tumour marker
 PT for anti-cancer agents -
 XX
 PS Claim 1; Page 2870-2871; 2979pp; Japanese.
 XX
 XX The invention relates to novel genes (AAI93926-AAI97963) expressed in
 CC human neuroblastoma. The nucleic acids are applicable as a probe or
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
 CC susceptibility indicators or tumour markers for anti-cancer agents. The
 CC gene information for diagnosing prognosis is related to factors similar
 CC to that for N-myc and TrkA genes.
 CC
 SQ Sequence 707 BP; 200 A; 129 C; 149 G; 224 T; 5 other;
 Query Match 92.0%; Score 18.4; DB 22; Length 707;
 Best Local Similarity 95.0%; Pred. No. 9.8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTTCACCCAGATGTCATTC 20
 |||||
 Db 431 TTTCACCCAGATGTCATTC 450
 RESULT 9
 ABA93211
 ID ABA93211 standard; DNA; 1311 BP.
 XX
 AC ABA93211;
 XX
 DT 17-APR-2002 (first entry)
 XX
 DE Coriolus versicolor aldo/ketoreductase encoding DNA SEQ ID NO:1.
 XX
 XX
 KW Aldo/ketoreductase; white-rot basidiomycete; methylbenzothioephene; AAD;
 KW aryl-alcohol dehydrogenase; enzyme; gene; ds.
 XX
 OS Coriolus versicolor.
 XX
 FH Key Location/Qualifiers
 FT CDS 354..1229
 FT /*tag= a
 FT /product= "aldo/ketoreductase"
 XX
 XX JP2001321171-A.
 PN
 XX
 XX 20-NOV-2001.
 PD
 XX
 PF 21-MAR-2000; 2000JP-0078691.
 XX
 XX 09-MAR-2000; 2000JP-0065559.
 PR
 XX
 PA (WARI/) WARIISHI H.
 PA (KUBI) KUBOTA CORP.
 XX
 XX WPI; 2002-158675/21.
 DR
 DR P-PSDB; ABB05467.
 XX
 XX A gene encoding a new protein and its use -
 PT
 XX
 PS Claim 1; Page 7-8; 12pp; Japanese.
 XX
 XX The present sequence encodes an aldo/ketoreductase (I) isolated from the
 CC white rot basidiomycete, Coriolus versicolor. The present invention also
 CC describes a method for detecting at least one sulphur-containing

CC hydrocarbon compound selected from methylbenzothiophenes in which, in a
 CC process of assaying a compound by the expression of (I), the increase in
 CC the expression of (I) shows that the compound is the objective compound.
 CC (I) and the gene encoding (I) can be used for decomposing noxious
 CC substances, particularly sulphur-containing heterocyclic compounds.
 XX
 SQ Sequence 1311 BP; 340 A; 332 C; 391 G; 248 T; 0 other;
 Query Match 85.0%; Score 17; DB 24; Length 1311;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TTCAACCCAGATGTCAT 18
 |||||
 Db 357 TTCAACCCAGATGTCAT 373
 RESULT 10
 ABA51579
 ID ABA51579 standard; DNA; 244 BP.
 XX
 AC ABA51579;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 XX Human breast cell single exon nucleic acid probe #10274.
 DE
 XX Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00662.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-496933/54.
 DR
 XX
 XX New spatially-addressable set of single exon nucleic acid probes,
 PT useful for measuring gene expression in sample derived from human
 PT breast, comprises number of single exon nucleic acid probes -
 XX
 PS Claim 4; SEQ ID NO 10274; 327pp + sequence listing; English.
 XX
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery, and for
 CC determining predisposition and/or prognosing breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 CC than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a single exon nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 244 BP; 50 A; 59 C; 36 G; 99 T; 0 other;

Query Match 84.0%; Score 16.8; DB 22; Length 244;
 Best Local Similarity 90.0%; Pred. No. 56;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
 |||||
 DB 118 TTTCACCGAGATGTCATTC 137

RESULT 11
 ABA36555
 ID ABA36555 standard; DNA; 244 BP.

XX AC ABA36555;

XX DT 23-JAN-2002 (first entry)

DE Probe #15021 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;

KM cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX OS Homo sapiens.

XX PN WO200157274-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00666.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488899/53.

XX PT Single exon nucleic acid probes for analyzing gene expression in human

XX PT hearts -

XX PS Claim 4; SEQ ID No 15021; 530bp; English.

XX XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging, the

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 244 BP; 50 A; 59 C; 36 G; 99 T; 0 other;

XX Query Match 84.0%; Score 16.8; DB 22; Length 244;

XX Best Local Similarity 90.0%; Pred. No. 56;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
 |||||
 DB 118 TTTCACCGAGATGTCATTC 137

RESULT 12
 AAK43716
 ID AAK43716 standard; DNA; 244 BP.

XX AC AAK43716;

XX DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 18273.

XX Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX OS Homo sapiens.

XX PN WO200157276-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US00668.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488900/53.

XX PT Human genome-derived single exon nucleic acid probes useful for

XX PT analyzing gene expression in human bone marrow -

XX PS Example 4; SEQ ID NO: 18273; 658bp + Sequence Listing; English.

XX XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is one of

CC the probes of the invention.

XX SQ Sequence 244 BP; 50 A; 59 C; 36 G; 99 T; 0 other;

XX Query Match 84.0%; Score 16.8; DB 22; Length 244;

XX Best Local Similarity 90.0%; Pred. No. 56;

XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20
 |||||
 DB 118 TTTCACCGAGATGTCATTC 137

RESULT 13
 ABA46482
 ID ABA46482 standard; DNA; 400 BP.

XX AC ABA46482;

XX DT 01-FEB-2002 (first entry)


```
DE Human breast cell single exon nucleic acid probe #5177.
XX Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
XX OS
XX PN WO200157271-A2.
XX PD
XX PF 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0234687.
XX PR 04-OCT-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-496933/54.
XX
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
XX Claim 1; SEQ ID NO 5177; 327pp + sequence listing; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 400 BP; 94 A; 97 C; 84 G; 125 T; 0 other;
SQ
Query Match 84.0%; Score 16.8; DB 22; Length 400;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTTCACACGATGGTCATTC 20
Db 344 TTTCACACGATGGTCATTC 363
RESULT 14
ABA26688
ID ABA26688 standard; DNA; 400 BP.
XX
XX ABA26688;
XX
XX 23-JAN-2002 (first entry)
XX
XX Probe #5154 for gene expression analysis in human heart cell sample.
XX
```

```
KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200157274-A2.
XX PD
XX PF 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00666.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0608408.
XX PR 03-AUG-2000; 2000US-0632366.
XX PR 21-SEP-2000; 2000US-0234687.
XX PR 27-SEP-2000; 2000US-0236359.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
XX Claim 1; SEQ ID No 5154; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosing diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 400 BP; 94 A; 97 C; 84 G; 125 T; 0 other;
SQ
Query Match 84.0%; Score 16.8; DB 22; Length 400;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTTCACACGATGGTCATTC 20
Db 344 TTTCACACGATGGTCATTC 363
RESULT 15
AAK30708
ID AAK30708 standard; DNA; 400 BP.
XX
XX AAK30708;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human bone marrow expressed single exon probe SEQ ID NO: 5265.
XX
XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
XX Homo sapiens.
XX OS
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
```

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XX 30-JAN-2001; 2001WO-US00668.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
DR WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human bone marrow -
XX
XX Example 4; SEQ ID NO: 5265; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention.
XX
SQ Sequence 400 BP; 94 A; 97 C; 84 G; 125 T; 0 other;

```

Search completed: January 12, 2003, 09:51:21
 Job time : 255 secs

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OY 1 TTTCACCGAGTGTGATTC 20
   |||||
Db 344 TTTCACCGAGTGTGATTC 363

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 09:46:10 ; Search time 47 Seconds
(without alignments)
130.501 Million cell updates/sec

Title: US-09-757-100B-18

Perfect score: 20

Sequence: 1 ttccaaccagatggtcattc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCtUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	20	100.0	20	3	US-09-377-310-18
2	20	100.0	3791	1	US-09-377-310-1
3	16.8	84.0	4465	1	US-08-180-195-1
4	16.8	84.0	4465	1	US-08-477-329-1
5	16.8	84.0	4465	2	US-08-475-458-1
6	16.8	84.0	4465	3	US-08-980-400-1
7	16.8	84.0	4465	4	US-09-583-459A-1
8	16.8	84.0	4465	4	US-09-583-210-1
9	16.8	84.0	4465	4	US-09-583-449A-1
10	16.8	84.0	4465	4	US-09-435-059-1
11	16.8	84.0	5427	1	US-08-168-917-1
12	16.8	84.0	5427	2	US-08-460-510-1
13	16.8	84.0	5427	2	US-08-460-490-1
14	16.8	84.0	5427	3	US-08-462-728-3
15	16.8	84.0	5427	4	US-08-461-917-3
16	16.8	84.0	5427	5	PCT-US92-00730-1
17	16.8	84.0	5427	5	PCT-US92-00862-1
18	15.8	79.0	7902	4	US-08-961-527-112
19	15.8	79.0	10223	4	US-08-961-527-73
20	15.2	76.0	3233	3	US-08-755-587-43
21	15.2	76.0	5313	4	US-09-329-920-1
22	15.2	76.0	6169	2	US-08-875-154-2
23	15.2	76.0	11385	2	US-08-639-501-1
24	15.2	76.0	11385	3	US-09-044-946-1
25	15.2	76.0	11385	3	US-09-044-908-1
26	15.2	76.0	87563	4	US-09-453-702B-57
27	15	75.0	15	3	US-09-377-310-38

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28 14.8 74.0 969 1 US-08-564-596B-4 Sequence 4, Appli
29 14.8 74.0 969 1 US-08-721-798A-1 Sequence 1, Appli
30 14.8 74.0 3266 4 US-08-485-511A-3 Sequence 3, Appli
C 31 14.8 74.0 8136 4 US-08-961-527-75 Sequence 75, Appl
C 32 14.8 74.0 246240 2 US-08-724-394A-20 Sequence 20, Appl
C 33 14.8 74.0 246240 2 US-08-724-394A-21 Sequence 21, Appl
C 34 14.8 74.0 246240 2 US-08-724-394A-22 Sequence 22, Appl
C 35 14.8 72.0 38 4 US-09-233-086-53 Sequence 53, Appl
36 14.4 72.0 1001 4 US-09-641-638-91 Sequence 91, Appl
37 14.4 72.0 1713 3 US-08-467-948A-1 Sequence 1, Appli
38 14.4 72.0 1713 3 US-08-467-947A-1 Sequence 1, Appli
39 14.4 72.0 1960 4 US-09-178-252-19 Sequence 19, Appl
C 40 14.4 72.0 2580 2 US-08-887-798-1 Sequence 1, Appli
41 14.4 72.0 3489 4 US-09-178-252-20 Sequence 20, Appl
42 14.2 71.0 20 3 US-09-357-071-39 Sequence 39, Appl
43 14.2 71.0 150 2 US-08-250-346-1 Sequence 1, Appli
44 14.2 71.0 267 4 US-09-696-569-7 Sequence 7, Appli
45 14.2 71.0 536 4 US-09-347-819-7 Sequence 7, Appli

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ALIGNMENTS

```

RESULT 1
US-09-377-310-18
; Sequence 18, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-18

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Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTTCACACAGATGGTCATTC 20
|||||
DB 1 TTTCACACAGATGGTCATTC 20
|||||

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RESULT 2
US-09-377-310-1/c
; Sequence 1, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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NAME/KEY: CDS
LOCATION: (233)..(3391)
PUBLICATION INFORMATION:
JOURNAL: DNA
VOLUME: 12
ISSUE: 9
PAGES: 823-830
DATE: 1993-11
DATABASE ACCESSION NUMBER: L13616/Genbank
DATABASE ENTRY DATE: 1995-01-02
US-09-377-310-1

Query Match 100.0%; Score 20; DB 3; Length 3791;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTCACCGATGGTCATTC 20
Db 3529 TTTCACCGATGGTCATTC 3510

RESULT 3
US-08-180-195-1/c
Sequence 1, Application US/08180195
Patent No. 5567584
GENERAL INFORMATION:
APPLICANT: Sledziwski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180.195
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634.510
FILING DATE:
APPLICATION NUMBER: US 07/146.877
FILING DATE: 22-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/347.291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 3990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4465 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N

ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Skin
CELL TYPE: fibroblasts
IMMEDIATE SOURCE:
CLONE: pr-rx1
FEATURE:
NAME/KEY: CDS
LOCATION: 354..3671
OTHER INFORMATION:
US-08-180-195-1

Query Match 84.0%; Score 16.8; DB 1; Length 4465;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TTTCACCGATGGTCATTC 20
Db 1263 TTTCACCGATGGTCATTC 1244

RESULT 4
US-08-477-329-1/c
Sequence 1, Application US/08477329
Patent No. 5750375
GENERAL INFORMATION:
APPLICANT: Sledziwski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindsvogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477.329
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4465 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Skin
CELL TYPE: fibroblasts
IMMEDIATE SOURCE:
CLONE: pr-rx1

FEATURE: CDS
NAME/KEY: 354...3671
LOCATION: 354...3671
OTHER INFORMATION:
US-08-477-329-1

Query Match 84.0%; Score 16.8; DB 1; Length 4465;

Best Local Similarity 90.0%; Pred. No. 13;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGTCATTC 20

Db 1263 TTTCATCCTGATGTCATTC 1244

RESULT 5

US-08-475-458-1/c

Sequence 1, Application US/08475458

Patent No. 5843725

GENERAL INFORMATION:

APPLICANT: Siedziwski Ph.D., Andrzej Z

APPLICANT: Bell, Lillian A.

APPLICANT: Kindsvogel Ph.D., Wayne R.

TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,458

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.446D5

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4465 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

DEVELOPMENTAL STAGE: Adult

TISSUE TYPE: Skin

CELL TYPE: fibroblasts

IMMEDIATE SOURCE:

CLONE: pr-rX1

FEATURE:

NAME/KEY: CDS

LOCATION: 354...3671

OTHER INFORMATION:

US-08-475-458-1

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 2; Length 4465;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGTCATTC 20

Db 1263 TTTCATCCTGATGTCATTC 1244

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGTCATTC 20

Db 1263 TTTCATCCTGATGTCATTC 1244

RESULT 6

US-08-980-400-1/c

Sequence 1, Application US/08980400

Patent No. 6018026

GENERAL INFORMATION:

APPLICANT: Siedziwski Ph.D., Andrzej Z

APPLICANT: Bell, Lillian A.

APPLICANT: Kindsvogel Ph.D., Wayne R.

TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/980,400

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/477,329

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.446C6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4465 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: N

ANTI-SENSE: N

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

DEVELOPMENTAL STAGE: Adult

TISSUE TYPE: Skin

CELL TYPE: fibroblasts

IMMEDIATE SOURCE:

CLONE: pr-rX1

FEATURE:

NAME/KEY: CDS

LOCATION: 354...3671

OTHER INFORMATION:

US-08-980-400-1

Query Match

Best Local Similarity 84.0%; Score 16.8; DB 3; Length 4465;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGTCATTC 20

Db 1263 TTTCATCCTGATGTCATTC 1244

Db 1263 TTTCATCCTGATGTCATTC 1244

RESULT 7

US-09-583-459A-1/c
Sequence 1, Application US/09583459A
Patent No. 6291212
GENERAL INFORMATION:
APPLICANT: Siegfiewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindavogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
TITLE OF INVENTION: FUSIONS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,459A
FILING DATE: 30-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,510
FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4465 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Skin
CELL TYPE: fibroblasts
IMMEDIATE SOURCE:
CLONE: pr-ix1
FEATURE:
NAME/KEY: CDS
LOCATION: 354..3671
OTHER INFORMATION:
US-09-583-459A-1

Query Match 84.0%; Score 16.8; DB 4; Length 4465;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACCAAGATGTCATTC 20
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RESULT 8

US-09-583-210-1/c
Sequence 1, Application US/09583210
Patent No. 6291646
GENERAL INFORMATION:
APPLICANT: Siegfiewski Ph.D., Andrzej Z
APPLICANT: Bell, Lillian A.
APPLICANT: Kindavogel Ph.D., Wayne R.
TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
TITLE OF INVENTION: FUSIONS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,210
FILING DATE: 30-MAY-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,510
FILING DATE: 27-DEC-1990
APPLICATION NUMBER: US 07/146,877
FILING DATE: 22-JAN-1988
APPLICATION NUMBER: US 07/347,291
FILING DATE: 02-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Maki J.D., David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 990008.446C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4465 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Skin
CELL TYPE: fibroblasts
IMMEDIATE SOURCE:
CLONE: pr-ix1
FEATURE:
NAME/KEY: CDS
LOCATION: 354..3671
OTHER INFORMATION:
US-09-583-210-1

Query Match 84.0%; Score 16.8; DB 4; Length 4465;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACCAAGATGTCATTC 20
|||||

Db 1263 TTTCATCCTGATGGTCATTC 1244
|||||
|||||

RESULT 9
US-09-583-449A-1/c
; Sequence 1, Application US/09583449A
; Patent No. 6300099
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
; TITLE OF INVENTION: AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,449A
; FILING DATE: 30-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,510
; FILING DATE: 27-DEC-1990
; APPLICATION NUMBER: US 07/146,877
; FILING DATE: 22-JAN-1988
; APPLICATION NUMBER: US 07/347,291
; FILING DATE: 02-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki J.D., David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Adult
; TISSUE TYPE: Skin
; CELL TYPE: fibroblasts
; IMMEDIATE SOURCE:
; CLONE: pr-rx1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 354..3671
; OTHER INFORMATION:
US-09-583-449A-1
Query Match 84.0%; Score 16.8; DB 4; Length 4465;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
|||||
Db 1263 TTTCATCCTGATGGTCATTC 1244
|||||
|||||
RESULT 10
US-09-435-059-1/c
; Sequence 1, Application US/09435059
; Patent No. 6323323
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
; APPLICANT: Bell, Lillian A.
; APPLICANT: Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS AND BIOLOGICAL
; TITLE OF INVENTION: FUSIONS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/435,059
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,329
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.446C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: Adult
; TISSUE TYPE: Skin
; CELL TYPE: fibroblasts
; IMMEDIATE SOURCE:
; CLONE: pr-rx1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 354..3671
; OTHER INFORMATION:
US-09-435-059-1
Query Match 84.0%; Score 16.8; DB 4; Length 4465;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
|||||
Db 1263 TTTCATCCTGATGGTCATTC 1244
|||||

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RESULT 11
US-08-168-917-1/c
; Sequence 1, Application US/08168917
; Patent No. 5686572
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Williams, Jaime A.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND
; STREET: Stuart Street Tower, 20th Floor \ One Market
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/168,917
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: 12418-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gti10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3504
; US-08-168-917-1

Query Match      84.0%; Score 16.8; DB 1; Length 5427;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

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; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Williams, Jaime A.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
; STREET: One Market Plaza, Stuart Street Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-001430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; STRAIN: lambda gti10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3504
; US-08-460-510-1

Query Match      84.0%; Score 16.8; DB 2; Length 5427;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
US-08-460-490-1/c
; Sequence 1, Application US/08460490
; Patent No. 5891652
; GENERAL INFORMATION:
; APPLICANT: Wolf, David
; APPLICANT: Tomlinson, James E.
; APPLICANT: Fretto, Larry J.
; APPLICANT: Giese, Neill A.
; APPLICANT: Escobedo, Jaime A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Williams, Jaime A.
; TITLE OF INVENTION: DOMAINS OF EXTRACELLULAR REGION OF HUMAN
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR POLYPEPTIDES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW
```


STREET: One Market Plaza, Steuart Street Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,490
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-001420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5427 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
STRAIN: lambda gt10
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3504
US-08-460-490-1

Query Match 84.0%; Score 16.8; DB 2; Length 5427;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
||||| ||||| ||||| ||||| |||||
Db 1096 TTTCATCCTGATGGTCATTC 1077

RESULT 14
US-08-462-728-3/c
Sequence 3, Application US/08462728
Patent No. 6043211
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower, 20th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,728
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-267-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5427 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 187..3507
US-08-462-728-3

Query Match 84.0%; Score 16.8; DB 3; Length 5427;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTCACACGATGGTCATTC 20
||||| ||||| ||||| ||||| |||||
Db 1096 TTTCATCCTGATGGTCATTC 1077

RESULT 15
US-08-461-917-3/c
Sequence 3, Application US/08461917
Patent No. 6372438
GENERAL INFORMATION:
APPLICANT: WILLIAMS, Lewis T.
APPLICANT: ESCOBEDO, Jaime A.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market, Steuart Street Tower, 20th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,917
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/309,322
FILING DATE: 10-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/151,414
FILING DATE: 02-FEB-1988
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-267-2-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/326-2400
TELEFAX: 415/326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..3507
; US-08-461-917-3
    
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Query Match      84.0%; Score:16.8; DB 4; Length 5427;
Best Local Similarity 90.0%; Pred. No.13;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
    
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Qy 1 TTCAACCGATGTCATTC 20
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Db 1096 TTTCATCCTGATGTCATTC 1077
    
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Search completed: January 12, 2003, 11:11:01
 Job time : 50 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 10:38:40 ; Search time 56 Seconds
(without alignments)
157.180 Million cell updates/sec

Title: US-09-757-100B-18
Perfect score: 20
Sequence: 1 ttccaaccagatgggtcattc 20
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues

Total number of hits satisfying chosen parameters: 778172

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_5/prodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_5/prodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_5/prodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_5/prodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_5/prodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_5/prodata/2/pubpna/PCTU5_PUBCOMB.seq.*
- 7: /cgn2_5/prodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_5/prodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_5/prodata/2/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_5/prodata/2/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_5/prodata/2/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_5/prodata/2/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_5/prodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_5/prodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	20	100.0	20	10	US-09-757-100B-18	Sequence 18, Appl
2	20	100.0	550	9	US-09-736-457-981	Sequence 981, App
3	20	100.0	550	9	US-09-902-941-981	Sequence 981, App
4	20	100.0	550	9	US-09-849-626-981	Sequence 981, App
5	20	100.0	3791	10	US-09-757-100B-1	Sequence 1, Appli
6	16.8	84.0	244	10	US-09-864-761-21875	Sequence 21875, A
7	16.8	84.0	400	10	US-09-864-761-5154	Sequence 5154, Ap
8	16.8	84.0	528	10	US-09-864-761-16204	Sequence 16204, A
9	16.8	84.0	1683	10	US-09-866-510-23	Sequence 23, Appl
10	16.8	84.0	3321	10	US-09-866-510-13	Sequence 13, Appl
11	16.8	84.0	3321	10	US-09-866-510-17	Sequence 15, Appl
12	16.8	84.0	3321	10	US-09-866-510-17	Sequence 17, Appl
13	16.8	84.0	3321	10	US-09-866-510-19	Sequence 19, Appl
14	16.8	84.0	3321	10	US-09-866-510-21	Sequence 21, Appl
15	16.8	84.0	4465	9	US-09-955-363-1	Sequence 1, Appli
16	16.8	84.0	11036	10	US-09-070-927A-464	Sequence 464, App
17	16.8	84.0	32191	10	US-09-764-864-1678	Sequence 1678, Ap
18	15.8	79.0	476	10	US-09-867-701-6708	Sequence 6708, Ap
19	15.8	79.0	575	10	US-09-974-300-5353	Sequence 5353, Ap

ALIGNMENTS

RESULT 1

US-09-757-100B-18
; Sequence 18, Application US/09757100B
; Patent No. US20010034329A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-18

Query Match 100.0%; Score 20; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0;

QY 1 TTTCACACAGATGGTCATTC 20

Db 1 TTTCACACAGATGGTCATTC 20

RESULT 2

US-09-736-457-981
; Sequence 981, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

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; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 981
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-981
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Query Match          100.0%; Score 20; DB 9; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TTCAACCGAGATGTCATTC 20
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Db      195 TTCAACCGAGATGTCATTC 214
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RESULT 3
US-09-902-941-981
; Sequence 981, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darlick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNeibb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 981
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-981
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Query Match          100.0%; Score 20; DB 9; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TTCAACCGAGATGTCATTC 20
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Db      195 TTCAACCGAGATGTCATTC 214
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RESULT 4
US-09-849-626-981
; Sequence 981, Application US/09849626
; Publication No. US2002019769A1
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; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tonglong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 981
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-981
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Query Match          100.0%; Score 20; DB 9; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TTCAACCGAGATGTCATTC 20
        |||||
Db      195 TTCAACCGAGATGTCATTC 214
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RESULT 5
US-09-757-100B-1/C
; Sequence 1, Application US/09757100B
; Patent No. US20010034329A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3791
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (233)..(391)
; PUBLICATION INFORMATION:
; JOURNAL: DNA
; VOLUME: 12
; ISSUE: 9
; PAGES: 823-830
; DATE: 1993-11
; DATABASE ACCESSION NUMBER: L13616/Genbank
; DATABASE ENTRY DATE: 1995-01-02
US-09-757-100B-1
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Query Match          100.0%; Score 20; DB 10; Length 3791;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      3529 TTCAACCGAGATGTCATTC 3510
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RESULT 6
US-09-864-761-21875
; Sequence 21875, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21875
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121654.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P47144, EVALUE 3.50e-02
US-09-864-761-21875

Query Match 84.0%; Score 16.8; DB 10; Length 244;
Best Local Similarity 90.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TTTCACACGATGGTCATTC 20
Db 118 TTTCACACGATGTACATTC 137

RESULT 7
US-09-864-761-5154
; Sequence 5154, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5154
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121654.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
US-09-864-761-5154

Query Match 84.0%; Score 16.8; DB 10; Length 400;
Best Local Similarity 90.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TTTCACACGATGGTCATTC 20
Db 344 TTTCACACGATGTACATTC 363


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; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT FILING DATE: 2001-05-25
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3318)
US-09-866-510-15

Query Match      84.0%; Score 16.8; DB 10; Length 3321;
Best Local Similarity 90.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTCAACACGATGTCATTC 20
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Db 910 TTTCATCCTGATGGTCATTC 891

RESULT 12
US-09-866-510-17/c
; Sequence 17, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT FILING DATE: 2001-05-25
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3318)
US-09-866-510-17

Query Match      84.0%; Score 16.8; DB 10; Length 3321;
Best Local Similarity 90.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTCAACACGATGTCATTC 20
||||| ||||| ||||| |||||
Db 910 TTTCATCCTGATGGTCATTC 891

RESULT 13
US-09-866-510-19/c
; Sequence 19, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
```

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; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT FILING DATE: 2001-05-25
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3318)
US-09-866-510-19

Query Match      84.0%; Score 16.8; DB 10; Length 3321;
Best Local Similarity 90.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTCAACACGATGTCATTC 20
||||| ||||| ||||| |||||
Db 910 TTTCATCCTGATGGTCATTC 891

RESULT 14
US-09-866-510-21/c
; Sequence 21, Application US/09866510
; Patent No. US20020111304A1
; GENERAL INFORMATION:
; APPLICANT: KAZLAUSKAS, ANDRIUS
; APPLICANT: IKUNO, YASUSHI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING FIBROTIC DISEASES
; FILE REFERENCE: ERM-104.01
; CURRENT FILING DATE: 2001-05-25
; CURRENT APPLICATION NUMBER: US/09/866,510
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/250,747
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/289,103
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3318)
US-09-866-510-21

Query Match      84.0%; Score 16.8; DB 10; Length 3321;
Best Local Similarity 90.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTCAACACGATGTCATTC 20
||||| ||||| ||||| |||||
Db 910 TTTCATCCTGATGGTCATTC 891

RESULT 15
US-09-955-363-1/c
; Sequence 1, Application US/09955363
; Patent No. US20020173621A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski Ph.D., Andrzej Z
;                      Bell, Lillian A.
;                      Kindsvogel Ph.D., Wayne R.
; TITLE OF INVENTION: METHODS OF PRODUCING SECRETED RECEPTOR ANALOGS
;                      AND BIOLOGICALLY ACTIVE DIMERIZED POLYPEPTIDE
```

```

? NUMBER OF SEQUENCES: 36 FUSIONS
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Seed and Berry
? STREET: 6300 Columbia Center
? CITY: Seattle
? STATE: WA
? COUNTRY: USA
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.24
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/955,363
? FILING DATE: 18-Sep-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/634,510
? FILING DATE: <Unknown>
? APPLICATION NUMBER: US 07/347,291
? FILING DATE: 02-MAY-1989
? ATTORNEY/AGENT INFORMATION:
? NAME: Maki J.D., David J.
? REGISTRATION NUMBER: 31,392
? REFERENCE/DOCKET NUMBER: 990008.446C3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-622-4900
? TELEFAX: 206-682-6031
? TELEX: 3723836
? INFORMATION FOR SEQ ID NO: 1:
? .SEQUENCE CHARACTERISTICS:
? LENGTH: 4465 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEITICAL: N
? ANTI-SENSE: N
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? DEVELOPMENTAL STAGE: Adult
? TISSUE TYPE: Skin
? CELL TYPE: Fibroblasts
? IMMEDIATE SOURCE:
? CLONE: PR-rx1
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 354..3671
? OTHER INFORMATION:
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
? US-09-955-363-1
Query Match 84.0%; Score 16.8; DB 9; Length 4465;
Best Local Similarity 90.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
QY 1 TTTCACCGATGCTCATTC 20
|||||
DB 1263 TTTCATCCGATGCTCATTC 1244

```

Search completed: January 12, 2003, 12:08:34
Job time : 59 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2003, 09:45:15 ; Search time 1993 Seconds
(without alignments)
162.524 Million cell updates/sec

Title: US-09-757-100B-18
Perfect score: 20
Sequence: 1 tttaaccagtggtcattc 20
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pin:*
- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match	Length	Description

C 1	20	100.0	285	12 BF997449
C 2	20	100.0	351	14 R32551
C 3	20	100.0	392	10 AV709841
C 4	20	100.0	412	10 BE092864
C 5	20	100.0	416	14 R89170
C 6	20	100.0	424	10 AV724065

C	7	20	100.0	425	10	BE566855
C	8	20	100.0	429	10	AW136503
C	9	20	100.0	432	9	AA983514
C	10	20	100.0	447	13	BM664187
C	11	20	100.0	462	14	N42230
C	12	20	100.0	481	9	AI341506
C	13	20	100.0	492	12	BF084847
C	14	20	100.0	492	13	BG986106
C	15	20	100.0	527	9	AI016118
C	16	20	100.0	532	9	AA404694
C	17	20	100.0	569	9	AI380178
C	18	20	100.0	585	14	BM790849
C	19	20	100.0	598	9	AA453479
C	20	20	100.0	610	10	AW003490
C	21	20	100.0	632	12	BF669338
C	22	20	100.0	648	10	AW992843
C	23	20	100.0	648	17	AG060293
C	24	20	100.0	676	12	BF691197
C	25	20	100.0	682	10	AW992847
C	26	20	100.0	690	17	AQ424326
C	27	20	100.0	693	12	BF978799
C	28	20	100.0	716	12	BF701452
C	29	20	100.0	722	10	BE567556
C	30	20	100.0	769	14	BQ438629
C	31	20	100.0	771	10	AV726076
C	32	20	100.0	808	10	BE380127
C	33	20	100.0	824	12	BF665639
C	34	20	100.0	844	12	BF241766
C	35	20	100.0	849	12	BG528906
C	36	20	100.0	852	10	BE617048
C	37	20	100.0	872	12	BF675982
C	38	20	100.0	882	12	BF217100
C	39	20	100.0	885	12	BF211871
C	40	20	100.0	888	12	BF698361
C	41	20	100.0	896	12	BF690762
C	42	20	100.0	906	12	BF213328
C	43	20	100.0	908	12	EG110386
C	44	20	100.0	930	12	BG617438
C	45	20	100.0	972	13	BI917958

ALIGNMENTS

RESULT 1
BF997449/c
LOCUS BF997449 285 bp mRNA linear EST 23-JAN-2001
DEFINITION CM0-GN0100-081100-576-a05 GN0100 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF997449
VERSION BF997449.1 GI:12403772
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 285)
AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CM0&c2=CM0-GN0100-081100-576-a05&c3=2000-11-08&c4=1)
 Seq primer: puc18 forward
 High quality sequence start: 10
 High quality sequence stop: 285.

FEATURES

source

```

1..285
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0100"
/dev_stage="Adult"
/notes="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
/site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

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BASE COUNT

```

71 a 69 c 46 g 99 t

```

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 285;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20

Db 163 TTTCACCGAGATGTCATTC 144

RESULT 2

R32551/c 351 bp mRNA linear EST 28-APR-1995
 LOCUS YH54D07.r1 Soares placenta NB2HP Homo sapiens cDNA clone
 DEFINITION IMAGE:133549.5 similar to gb:L05186 FOCAL ADHESION KINASE (HUMAN
); mRNA sequence.

ACCESSION R32551
 VERSION R32551.1 GI:788394
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 351)
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Ritzkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)

TITLE

JOURNAL

COMMENT

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

Insert Size: 691
 High quality sequence stops: 299
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 691 Std Error: 0.00
 Seq primer: M13RPI
 High quality sequence stop: 299.

FEATURES

source

```

1..351
/organism="Homo sapiens"
/db_xref="GDB:539375"
/db_xref="taxon:9606"
/clone="IMAGE:133549"

```

```

/clone_lib="Soares placenta NB2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: placenta; Vector: p773D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
ACTGGAAGATTGCGCGCCGACAGGATTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773D vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

```

BASE COUNT

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100 a 66 c 65 g 120 t

```

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 351;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20

Db 104 TTTCACCGAGATGTCATTC 85

RESULT 3

AV709841/c 392 bp mRNA linear EST 09-OCT-2000
 LOCUS AV709841 ADC Homo sapiens cDNA clone ADCAG11 5', mRNA sequence.
 DEFINITION AV709841
 ACCESSION AV709841
 VERSION AV709841.1 GI:10727915
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 392)
 Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Ou, J., Gao, X., Cheng, Z., Xu, Z.,
 Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
 Homo sapiens cDNA ADC clones
 Unpublished (2000)

TITLE

Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.
 Location/Qualifiers

FEATURES

source

```

1..392
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCAG11"
/clone_lib="ADC"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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BASE COUNT 107 a 85 c 82 g 116 t 2 others
 ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 392;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCACCGAGATGTCATTC 20

Db 173 TTTCACCGAGATGTCATTC 154

COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..424
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTBA1P1"
/clone_1ib="HTB"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 118 a 90 c 80 g 136 t

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
|||||
DB 215 TTTCAACGAGATGTCATTC 196

RESULT 7
BE566855/c 425 bp mRNA linear EST 15-AUG-2000
LOCUS 601339461P1 NIH_MGC_53 Homo sapiens CDNA clone IMAGE:3681878 5',
DEFINITION mRNA sequence.
ACCESSION BE566855
VERSION BE566855.1 GI:9810575
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 425)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC364 row: 1 column: 15
High quality sequence stop: 421.
Location/Qualifiers
1..425
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3681878"
/clone_1ib="NIH_MGC_53"
/tissue_type="Carcinoma, cell line"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccgcccgc); Site_2: SfiI (ggccatctggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATATGACC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCGCGCATG-3' (30 BN-3'
(where B = A, C, or G and N = A, C, G, or T) Average
insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 117 a 118 c 91 g 99 t

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
|||||
DB 376 TTTCAACGAGATGTCATTC 357

RESULT 8
AM136503 429 bp mRNA linear EST 29-OCT-1999
LOCUS UI-H-B11-acx-e-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens CDNA clone
DEFINITION IMAGE:2715763 3', mRNA sequence.
ACCESSION AM136503
VERSION AM136503.1 GI:6140563
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 429)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. CDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdtp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2715763"
/clone_1ib="NCI CGAP Sub3"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI CGAP Sub3 library is a subtracted library derived from
the NCI CGAP Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI CGAP libraries: NCI_CGAP_C04
, NCI_CGAP_P122, NCI_CGAP_P128, NCI_CGAP_C010,
NCI_CGAP_C016, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_C08, NCI_CGAP_C011, NCI_CGAP_Let12,
NCI_CGAP_Br23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonides 1322376-1323911, 1456008-1456775
, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLM 3338-3342
, 3722-3729, 3776-3778 (IMAGE Clonides 1323912-1325831,
1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
LLM 3575-3582, 3851-3854 (IMAGE Clonides 1414920-1417991,
1520904-1524239); NCI_CGAP_GC4 pool 1 LLM 3164-3167,

3716-3720, 3733-3735 (IMAGE Clones) 1257096-1258631,
1459064-1470983, 1475552-1476743; NCI_CGAP_P22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones)
985608-986759, 1101192-1101959, 1217928-1220615;
NCI CGAP Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
Clones) 1057416-1061255, 1144584-1145351. Subtraction
was performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches to Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG LIB=NCI CGAP GC4
TAG TISSUE=Germ Cell
TAG_SEQ=AAATC"
BASE COUNT 113 a 80 c 105 g 131 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 429;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCAACACGATGTCATTC 20
|||||
Db 108 TTTCAACACGATGTCATTC 127
|||||

RESULT 9
AA983514 432 bp mRNA linear EST 27-AUG-1998
LOCUS or41g10.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1598466 3'
DEFINITION similar to gb:U05186 FOCAL ADHESION KINASE (HUMAN);, mRNA sequence.
ACCESSION AA983514
VERSION AA983514.1 GI:3162039
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-femail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1419 Std Error: 0.00
Seq primer: -40m13 fwd, RT from Amersham.

FEATURES
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1. .432
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1598466"
/clone_lib="NCI_CGAP_GC3"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 116 a 81 c 114 g 121 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 432;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCAACACGATGTCATTC 20
|||||
Db 91 TTTCAACACGATGTCATTC 110
|||||

RESULT 10
BM664187 447 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-C11-agg-d-10-0-UI.s1 UI-E-C11 Homo sapiens cDNA clone
DEFINITION UI-E-C11-agg-d-10-0-UI 3', mRNA sequence.
ACCESSION BM664187
VERSION BM664187.1 GI:18970113
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-22, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1. .447
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-C11-agg-d-10-0-UI"
/clone_lib="UI-E-C11"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-C11 is a normalized cDNA library containing the
following tissue(s): RPE and Choroid. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is ACCTA.
This library was created for the program, Gene Discovery
in the Visual System, supported by National Eye Institute
(NEI).
TAG LIB=UI-E-C11
TAG_TISSUE=RPE and Choroid
TAG_SEQ=ACCTA"
BASE COUNT 127 a 81 c 103 g 136 t
ORIGIN

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 447;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
 |||
 Db 157 TTTCAACGAGATGTCATTC 176

RESULT 11

LOCUS M42230/c 462 bp mRNA linear EST 24-JAN-1996
 DEFINITION yw71h06.r1 Soares placenta_8to9weeks_2NBHP8to9w Homo sapiens cDNA
 similar to gb:L05186 FOCAL ADHESION KINASE (HUMAN);, mRNA sequence.

ACCESSION M42230
 VERSION M42230.1 GI:1166261
 KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens
 human.

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 462)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maiz, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 330
 Source: IMAGE Consortium, LINT
 This clone is available royalty-free through LINT; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: T7
 High quality sequence stop: 330.

FEATURES

source

1..462
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="GDB:387333"
 /db_xref="taxon:9606"
 /clone="IMAGE:257723"
 /clone_lib="Soares_placenta_8to9weeks_2NBHP8to9w"
 /dev_stage="two placentae: one from 8 weeks and another
 from 9 weeks post conception"
 /lab_host="DH10B (ampicillin resistant)"
 /note="organ: placenta; Vector: pRTT3D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCACATCGAGTGAAGCGGCGCGCGATTTTCTTTTCTTTT 3']
 TGTTCACATCGAGTGAAGCGGCGCGCGATTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRTT3 vector
 (Pharmacia). Library constructed by Bento Soares and
 M. Fatima Bonaldo."

BASE COUNT 137 a 96 c 89 g 139 t 1 others

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 462;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
 |||
 Db 193 TTTCAACGAGATGTCATTC 174

RESULT 12

LOCUS A1341506 481 bp mRNA linear EST 15-FEB-1999
 DEFINITION qx92a12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:200950 3'
 similar to gb:L05186 FOCAL ADHESION KINASE (HUMAN);, mRNA sequence.

ACCESSION A1341506
 VERSION A1341506.1 GI:4078433
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 481)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINT at:
 www-bio.lnl.gov/bbip/image/image.html
 Insert length: 686 Std Error: 0.00
 Seq primer: -40UP from G1bco
 High quality sequence stop: 445.

FEATURES

source

1..481
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:200950"
 /clone_lib="NCI-CGAP_GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pRTT3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
 from the normalized library NCI-CGAP_GC4 was prepared, and
 89 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneIDs
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 128 a 98 c 123 g 132 t

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 481;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCAACGAGATGTCATTC 20
 |||
 Db 92 TTTCAACGAGATGTCATTC 111

RESULT 13

LOCUS BF084847/c 492 bp mRNA linear EST 18-OCT-2000
 DEFINITION PM2-DT0042-100900-003-g03 DT0042 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF084847
 VERSION BF084847.1 GI:10878677
 KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 492)

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL MEDLINE COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM2-DT0042-100
900-003-g03&t3=2000-09-10&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 492.

FEATURES
source
1. .492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DT0042"
/dev_stage="Adult"
/note="Organ: denis drash; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
139 a 114 c 99 g 140 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCACACGATGGTCATTC 20
|||||
Db 325 TTTCACACGATGGTCATTC 306

RESULT 14
BG986106/c
LOCUS BG986106 492 bp mRNA linear EST 13-JUN-2001
DEFINITION PM2-DT0042-190201-005-g03 DT0042 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG986106
VERSION BG986106.1 GI:14390176
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-DT0042-190201-005-g03&t3=2001-02-19&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 492.

FEATURES
source
1. .492
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DT0042"
/dev_stage="Adult"
/note="Organ: denis drash; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
139 a 114 c 99 g 140 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 492;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCACACGATGGTCATTC 20
|||||
Db 325 TTTCACACGATGGTCATTC 306

RESULT 15
AI016118
LOCUS AI016118 527 bp mRNA linear EST 27-AUG-1998
DEFINITION ct34g07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618716 3' similar to gb:L05186 FOCAL ADHESION KINASE (HUMAN);, mRNA sequence.
ACCESSION AI016118
VERSION AI016118.1 GI:3230454
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 752 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 344.
Location/Qualifiers
1. .527
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

/clone="IMAGE:1618716"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGCGCCCAATTTT TTT TTT TTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

BASE COUNT 135 a 104 c 134 g 154 t

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 527;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCACACAGATGTCATTC 20
 |||||
 Db 100 TTTCACACAGATGTCATTC 119

Search completed: January 12, 2003, 11:09:54
 Job time : 1997 secs